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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      July 10, 2003, 18:15:27; Search time 63.3034 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2185239 seqs, 1125999159 residues
                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-087-631B-4
                                                                                                                                                                                                      Query
 68.0
68.0
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64.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1
                                                                                                                                                                                   Length
                                                                                                                                                                                     DB
                                                                                                                                                                                     Ä
                   ABL70738
AAC76076
AAH90080
AAK68321
AAS05390
ABK64829
AAAO0522
AAAZ27923
                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (without alignments)
1067.241 Million cell updates/sec
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Human benign prost
Human colon cancer
Canine B7-2S prote
Complementary stra
                                                                                       Corn tassel-derive
Human ORFX ORF1631
Human bone marrow
Human immune/haema
                                                                                                                                                                                 Description
                                                                      Human titin (conne
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
ABL70738/c
ID ABL70738 standard; cDNA; 340 BP.
XX
AC ABL70738;
XX
DT 14-MAY-2002 (first entry)
XX
DE Corn tassel-derived polynucleotide
XX
                                                                                                                                                                                                                                                                                                                                                                                                                     Corn tassel-derived polynucleotide (cdps) SEQ ID NO:112.
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Database :

Searched:

Scoring table: Sequence: Title: Perfect score: Run on:

				•		
Breast cancer rela	ABL64091	24	2330	61.3	18.4	5
	ABL63694	24	2330	61.3	18.4	4
Streptococcus pneu	AAV72649	20	1526	Ë	18.4	ü
s pn	AAV82062	20	1476	۲	18.4	12
Ė	ABK33160	24	1329	۳	18.4	1
Streptococcus pneu	AAZ48094	21	1329	61:3	18.4	0
NA encoding	AAT98600	19	1297	:	18.4	39
	AAH65710	22	1272	۳	18.4	
Streptococcus pneu	AAV72650	20	1260	۳	18.4	37
	AAF21784	21	796		18.4	8
breast	AAT51183	18	787	1	18.4	8
	AAI93778	22	783	Ľ	18.4	4
Human persyn gene	AAX29997	20	720	۲	18.4	ä
. Breast cancer rela	ABL63343	24	550	7	18.4	ະ
Human HBGBA67A DNI	AAA39470	21	550	Ľ	18.4	31
	AAV42669	19	550	۲.	18.4	ö
secre	AAC02234	21	313	۲.	18.4	8
gamma	AAX04875	20	223		18.4	8
Human brain Expres	AAQ61427	14	223	۳	18.4	27
Human gamma-synuci	AAD14356	22	210	۳	18.4	8
DNA encoding nove	AAS66460	23	717	ν.	18.6	ៜ
Rat sequence diffe	ABK62829	24	531	'n	18.6	24
	AAA31281	21	485	2	18.8	23
Human immune/haema	AAK69721	22	16086	Ψ	. 19	2
Human musculoskele	AAL36020	22	. 16086	ω.	19	21
Drosophila melanoo	ABL12988	23	12768	ü	19	8
Human immune/haema	AAK67034	22	5057	ω	19	9
DNA encoding nove	AAS86898	23	2679	ω	19	8
Probe, SK535, for	AAT32453	17	33	ü	19	7
4	AAH25420	22	31	ω	19	9
B7-2	AAZ27914	20	1897	٠.	ø	5
B7-2 ₽	AAZ27913	20	1897	٠.	ò	4
B7-2S	AAZ27922	20	1795	٠.	9	ω
Canine B7-2S prote	2792	20	1795		19.4	2
mentar	AAZ27916	20	987	64.7		Ξ
Canine B7-2 protei	AAZ27915	20	987	64.7		0

## ALIGNMENTS

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D X	PI	PA	PA	PA	XX	PR	X	ΡF	×	PD	X	PΝ	×	SO	X	KW .	X	KW	XΨ	2
WPI: 2002-163647/21.	Lalgudi RV, Ito LY, Sherman BK;	(SHER/) SHERMAN B K.	(ITOL/) ITO L Y.	(LALG/) LALGUDI R V.		21-APR-1998; 98US-082567P.		16-APR-1999; 99US-0294093.		13-DEC-2001.		US2001051335-A1.		Zea mays.		multigene trait; plant breeding; corn tassel; gene; ss.	environmental adaptability; quality; yield; molecular marker;	inheritance; characteristic; growth; development; disease resistance;	Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs;	
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Result

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Matches
                                                                                                                                                                              antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antinnaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; josteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism, SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                            immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antihyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX ORF1631 polynucleotide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be transcript image, to clone regulatory elements for use in transformation exercis, to express a polypeptide, to identify, isolate or extend identifical or related corn tassel nucleic acid sequences from DNA as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC7607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC76076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences (1) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (or more) nucleic acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                      open reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGACACGGTACATGTTCATCTCATCTTCT .97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 BP; 102 A; 52;C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID 112; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                    cartilage damage; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                describes a purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1323
                                                                                                                                                                                                                                                                                                                                                                                        ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 G; 89 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corn tassel-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:3261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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CC which represent the human ORTX open reading frames 1 to 3161. The ORTX CC which represent the human ORTX open reading frames 1 to 3161. The ORTX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; CC immunostimulant; cardiant; thrombolytic; cosquiant; vasotropic; cc antidiabetic; hypotensive; dermatological; immunosuppressive; antitheumatic; CC antithflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antithflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antithflammatory; and antipartial; antiviral; antifungal; antirheumatic; CC antithflammatory; and antipartial; antiviral; antifungal; antirheumatic; CC antithflammatory; and antipartial; antiviral; antipungal; antirheumatic; CC antithflammatory; and antipartial; antiviral; antipungal; antipungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1323 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC74446 to AAC77606 encode the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0127607.
990S-0127636.
990S-0127728.
20000S-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2462; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leach
            239 A; 435
C; 343 G; 304 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame X,
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Matches Query Match Best Local 997 , ب 24; Similarity TGGACTCAGTCCTTGGTCATCTCACCTTCT TGGTCTCACTCCTTGGACTTGTCACCTTGT Conservative 68.0%; 0; Pred. No. 2 Mismatches 30 DВ 21; 6, Length Indels 1323; 0;

·Gaps

1026

밁 Q

AAH90080/ RESULT AAH90080 standard; cDNA; 1449 ВP

XX AX XX Human bone marrow 01-OCT-2001 AAH90080; (first entry) CDNA, SEQ ID NO: 324.

Human; bone marrow; antiinflammatory; cytostatic; antiviral; antibacterial; antifungal; anti-Hufy, himmunosuppressive; gene therapy; cytokine cell procell differentiation modulator; immune disorder; immunodeficiency HIV; cytokine cell proliferation; cmmune disorder; infection; c anti-HIV; haemostatic; neuroprotective;

Homo sapiens

WO200153453-A2

31-MAR-2000; 2000WO-US08621

05-OCT-2000

WO200058473-A2

thrombosis;

contraceptive;

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RESULT 4
AAK6837
ID AAK6
XX AAK6
AC AAK6
XX AAK6
DT 06-N
DT 06-N
DT 05-N
XX Huma
XX Cytc
XX Huma
XX Huma
XX Homc
XX Hom
X
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                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1449 BP; 334 A; 394 C; 446 G; 274 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in the bone marrow. The popolypeptide encoded by it are useful immune deficiencies and disorders. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ford JE, Boyle BJ, Tang YT, I
Ren F, Wang J, Werhman T, Xu
Zhao QA, Zhou P, Drmanac RT;
   31-JAN-2000; 2000US-0179065.
                                   17-JAN-2001; 2001WO-US01354.
                                                                  09-AUG-2001
                                                                                                                                                                cytostatic;
                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                    06-NOV-2001
                                                                                                                                                                                                                                                                                     AAK68321;
                                                                                                                                                                                                                                                                                                                    AAK68321 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488707/53.
P-PSDB; AAM00961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000;
09-JUL-2000;
                                                                                                   WO200157182-A2.
                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of 251 novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L4-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                      327
                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  TGGTCTCACTCCTTGGACTTGTCACCTTGT 298
                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0662191.
2000US-0693036.
2000US-0250583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-0598042.
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US34960
                                                                                                                                                                therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                    DNA; 15809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.4;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                     뫄.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polynucleotide and the useful in the treatment of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Asundi V,
Xue AJ, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang Y, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                    ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels.
                                                                                                                                                                                                        SEQ ID NO:23133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n R, Ma '
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç,
   25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
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25-SEP-2000;
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L4-AUG-2000;
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2000US-0232400.
2000US-0232401.
2000US-0233063.
2000US-0233064.
2000US-0233065.
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2000US-0184664.
2000US-0186350.
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2000US-0231968
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s-0236327.
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metastasis
           Nucleic
                   WPI; 2001-483426/52.
                              Rosen CA
                                       (HUMA-)
    acids encoding or preventing,
                                      HUMAN GENOME
                            Barash SC,
                                      SCI INC
human immune/hematopoietic antigen diagnosing and/or treating cancers
                            MS
  polypeptides, and
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The present sequence encoding for human titin (also known as connectin)

Disclosure; Page 35-57; 114pp; English.

Determining if a subject has or is at risk of developing a titin-related disease or condition, particularly heart failures, comprises detecting the presence of a mutation in the titin gene

gene

WPI; 2001-451869/48. P-PSDB; AAU05396.

Fishman

MC;

(GEHO ) GEN HOSPITAL CORP.

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AAS05390/c
ID AAS05390 standard; DNA; 81940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) cc proteins and polynucleotides may be used in the prevention, diagnosis and cexample, they may be used to treat disorders associated with inappropriate (I) expression. For cc expression by rectifying mutations or deletions in a pattent's genome cc supplement the pattents own production of (I). Additionally, (I) the nucleotides may be used to produce the secreted (I), by inserting cc polynucleotides may be used to produce the secreted (I), by inserting cc protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting cc diagnose and treat immune/haematopoietic-related diseases, especially cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703 csequences from the present invention. AAK54942 to AAK54550 and AAM82169 cc represent sequences used in the exemplification of the present invention.
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Best Local
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                                                                                                                                                                                       12-JAN-2000; 2000US-0175787
                                                                                                                                                                                                                12-JAN-2001; 2001WO-US01212.
                                                                                                                                                                                                                                                                     WO200151666-A1:
                                                                                                                                                                                                                                                                                                                                                                                       Human; titin;
titin-related
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human titin (connectin) gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS05390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15809 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK54951 to AAK64702 encode the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
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22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%;
idlarity 84.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                         connectin; pickwick mutation; cardiac specific exon; N2B;
disease; zebrafish; heart failure; heart disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 23133; 3071pp +
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 133..80913
                                                                                                                                                                                                                                                                                            /product= "titin"
                                                                                                                                                                                                                                                                                                          /*tag≒
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3658 A; 4263 C; 4050 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.6;
Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3838 T;
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ABK64829/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-)
                                                                                                                                                                                                                                                                                                                      WPI;
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                  progression of benign prostatic hyperplasia (BPH), or screening or identifying an agent that modulates the onset or progression. The method is based on changes in gene expression in BPH tissue from patients exhibiting different clinical states of prostate
                                                                                                               The invention
                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                          Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                   Munger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-2000;
05-JUN-2001;
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hyperplasia as compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified using the methods may be used to treat pati
or are at risk of developing heart disease, e.g. heart
                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                               Kulkarni P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2001US-0873319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostatic hyperplasia gene #724.
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                                                                                                             relates to a method of diagnosing (I) the onset or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostatic hyperplasia; BPH; prostate cancer; gene;
                                                                                                                                                            405-429;
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Pred: No. 1.
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                                                                  of BPH.
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                                             isolated
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Polynucleotide WPI; 2000-126369/11.

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Claim 1;

Page 302; 1097pp; English

AAA00010 to AAA02716 represent polynucleotides isolated

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Best Local
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to present information identifying the expression level in a tissue or cells, by comparing the expression level in the specification in the tissue or cells to the level of expression of gene in the database, and displaying the expression levels of at least one gene in the tissue or cell sample compared to the expression level in BPH. Agents using (II) are useful treating BPH or prostate cancer. ABK64106-ABK64860 represent human benign prostatic hyperplasia gene sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profil of BPH cells or BPH-11ke cell population, exposing the cells to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles.
                                                       Williams LT, Reinhard C,
                                                                                  Williams
                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09958675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oestrogen receptor-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer cell line polynucleotide sequence
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                                                                                                                                  (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                 27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                   13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oreast cancer; oestrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21155
                                  ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTACTGAGTCCTTGGTTATATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGACTCAGTCCTTGGTCATCTCACC
                               , Giese K,
Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                    Escobedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression levels of one
                                                                                                                                                                                                                                    98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
                                                                                                                                                                                                               98US-0105877
                                                                                                                                                                                                                                                                                                                                                                   99WO-US10602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pression levels of one or
that are differentially i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancerous state; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26373 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
Randazzo F,
Crkvenjakov F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor-positive breast cancer; therapy;
                                                                                  Innis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17097 C; 18901 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                       Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21130
                                                                                  Garcia PD,
                                  Dickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19569 T; 0
                                  Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dentification;
                                                             Pot D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                  Sudduth-Klinger
                                  Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product;
                                                             Kassam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IJ
          B, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                  Labat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    profile
                                                                                    Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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RESULT 8
AAZ27923/c
ID AAZ27923
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             The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding |nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autdimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases atomic dermatitis. They can be used in mammals such humans, dogs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                 New isolated B7 and CTLA4
                                                                                                                                                                                                                                                                                              treating,
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sim G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-мак-1998;
17-арк-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B7; CTLA4; T cell costimulatory protein; dog; cat; autoim allergic reaction; infectious disease; tumor development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HESK-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1|999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09947558-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sample derived from a cell suspected of being cancerous, where detect of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer; oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting at least one differentially expressed gene product in sample derived from a cell suspected of being cancerous, where compared to the compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes correlated with a cancerous state of a mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries constructed from human colon cancer cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                     1999-571822/48.
DB; AAY41078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         réjection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87-2S protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HESKA CORP.
                                                                                                                                                                                                                                  Page 114; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                         e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCCTCCATCTTGGGTCATCTCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGACTCAGTCCTTGGTCATCTCACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 BP; 70 A; 75 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                         S, Sellins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0078765.
98US-0062597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US06187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.78;
79.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840
                                                                                                                                                                                                                                                                                       nucleic acids, used to and atopic diseases
                                                                                                                                                                                                                                                                            and atopic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 G; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis; atopic dermatitis; ss
          products can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
          also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cat; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...
                                                                                                                                                                                                                                                                                                 develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentially
     be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present ially expressed ell, comprising duct in a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Ħe.

RESULT 10 AAZ27915/c ID AAZ27915 standard; DNA;

987 ВP 밁 Š

87

2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30

GTACTCTTTCCTTGGTCTGCTCACTTTCT

115

Best Matches

Local

Similarity

64.78; 79.38;

Score 19.4; Pred.

DB

20;

840;

Mismatches

, 6;

Indels Length

0;

Gaps

0

NO.

Conservative

Query Match

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RESULT 9
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                    The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or tracting diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor such as atopic dermatitis. They can be used in mammals such humans, dogs cats, cattle, sheep or pets. The products can also be used for detection, distanceies and description are producted and sheep contents.
 Sequence 840 BP; 214 A; 167 C;
                                                                                                                                                                        Claim 1; Page 115; 148pp; English.
                                                                                                                                                                                              New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases.
                                                                                                                                                                                                                                                  WPI; 1999-571822/48
                                                                                                                                                                                                                                                                                 Sim G,
                                                                                                                                                                                                                                                                                                                                        19-MAR-1998;
17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementary strand of canine B7-2S coding
                                                                                                                                                                                                                                                                                                            (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        W09947558-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B7; CTLA4; T cell costimulatory protein; allergic reaction; infectious disease; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ27924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ27924 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 840 BP; 278 A; 181 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            754 GTACTCTTTCCTTGGTCTGCTCACTTTCT
                                                                                                                                                                                                                                                                             Yang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGACTCAGTCCTTGGTCATCTCACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
23; Conserv
                              tle, sheep or pets.
and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                      98US-0078765.
98US-0062597.
                                                                                                                                                                                                                                                                                                                                                                              99WO-US06187.
                                                                                                                                                                                                                                                                               Sellins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation; arthritis; atopic dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 840 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 50,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
 181 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.4;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç;
278 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cat; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    canine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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8 x 5 5 5 5 5 5 5 5 5 5 8 x 8
Query Match
Best Local
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                                                                             B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious disease; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis; ss.
              W09947558-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 987 BP; 315 A; 215 C; 204 G; 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can expressed by standard recombinant methodology. The nucleic acid molecular expressed by standard recombinant methodology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated B7 and CTLA4 nucleic acids, used treating, e.g. autoimmune and atopic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-571822/48.
P-PSDB; AAY41076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sim G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris.
                                                Canis familiaris
                                                                                                                                                      Complementary strand of canine B7-2 coding sequence
                                                                                                                                                                                           20-DEC-1999
                                                                                                                                                                                                                              AAZ27916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1998;
17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine B7-2 protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ27915;
                                                                                                                                                                                                                                                                 AAZ27916 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HESK-) HESKA CORP
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                                                                                                                                                                                                                                                                                                                                                          901
                                                                                                                                                                                                                                                                                                                                                                       2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 102-103;
                                                                                                                                                                                                                                                                                                                                                      GTACTCTTTCCTTGGTCTGCTCACTTTCT 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sheep or pets. The products can also be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .98US-0078765
98US-0062597
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                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.4;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            987;
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RESULT 12
AAZ27921/c
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Query Match
Best Local S
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                              WPI; 1999-571822/48
P-PSDB; AAY41078.
                                                              Sim G, Yang S,
                                                                                                             19-MAR-1998;
17-APR-1998;
                                                                                                                                                                                                                                      B7; CTLA4; T cell costimulatory protein; allergic reaction; infectious disease; to graft rejection; inflammation; arthritis
                                                                                                                                                                                                                                                                                   Canine B7-2S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cats, cattle, sheep or pets. The products can also diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the encoded proteins can be used e.g. autoimmune diseases, allergic re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 103-104; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated B7 and CTLA4 nucleic acids, used treating, e.g. autoimmune and atopic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sim G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1998;
17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1999;
                                                                                   (HESK-) HESKA CORP.
                                                                                                                                               19-MAR-1999;
                                                                                                                                                                      23-SEP-1999
                                                                                                                                                                                            W09947558-A2
                                                                                                                                                                                                                  Canis familiaris.
                                                                                                                                                                                                                                                                                                          20-DEC-1999
                                                                                                                                                                                                                                                                                                                               AAZ27921;
                                                                                                                                                                                                                                                                                                                                                   AAZ27921 standard; DNA; 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 987 BP; 253 A; 204 C; 215 G; 315 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-571822/48
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                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                             GTACTCTTTCCTTGGTCTGCTCACTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                             98US-0078765
98US-0062597
                                                                                                                                               99WO-US06187
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98US-0062597
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                                                                Sellins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sellins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%; Score 19.4;
79.3%; Pred. No. 57;
                                                                                                                                                                                                                                                                                  encoding
                                                                  XS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergic reactions,
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                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                        arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for preventing or treating diseases,
                                                                                                                                                                                                                                                  n; dog; cat; auto
tumor developmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                        atopic dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                            cat; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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New isolated B7 and CTLA4 nucleic acids, used treating, e.g. autoimmune and atopic diseases

to develop products

Pred. No

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XX CCCCCCCCX PX P P P XX
          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                         Sequence
                                                                                        development, graft rejection, in such as atopic dermatitis. They
                                                                                                                                                                                               Claim 1; Page 112-114; 148pp; English.
                                                                                                                                                                                                                           New isolated B7 and CTLA4 nucleic acids, used treating; e.g. autoimmune and atopic diseases
                                                                                                                                                                                                                                                                           WPI; 1999-571822/48
                                                                                                                                                                                                                                                                                                          Sim G,
                                                                                                                                                                                                                                                                                                                                                            19-MAR-1998;
17-APR-1998;
                                                                                                                                                                                                                                                                                                                                    (HESK-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B7; CTLA4; T cell costimulatory protein; dog; allergic reaction; infectious disease; tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canine B7-2S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, catts, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1795 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nvention provides B7 and CTLA4 (T cell costimulatory proteins) ling nucleic acid molecules from dogs and cats. The proteins can be used by standard recombinant methodology. The nucleic acid molecules the encoded proteins can be used for preventing or treating diseases, autoimmune diseases, allergic reactions, infectious diseases, tumor
                                        1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.
                                                                                                                                                                                                                                                                                                                                  HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1999.
                                                                                                                                                                                                                                                                                                       Yang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Conser
                                                              and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTACTCTTTCCTTGGTCTGCTCACTTTCT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 109-111; 148pp; English.
                                                                          sheep or pets.
                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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98US-0062597
                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US06187
                                                                                                                                                                                                                                                                                                    Sellins KS;
                             490 A; 347 C; 366 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complementary DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 A; 366 C; 347 G; 490 T; 0 other;
       64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.78;
79.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1795
     Score 19.4;
                                                                      The products can
                                                                                   inflammation,
ey can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19.4;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                          592 T; 0 other;
    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atopic
                                                                             arthritic and atopic diseases in mammals such humans, dogs,
  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                         also
                                                                                                                                                                                                                                to develop products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
Length 1795;
                                                                    be' used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1795;
                                                                for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 canine;
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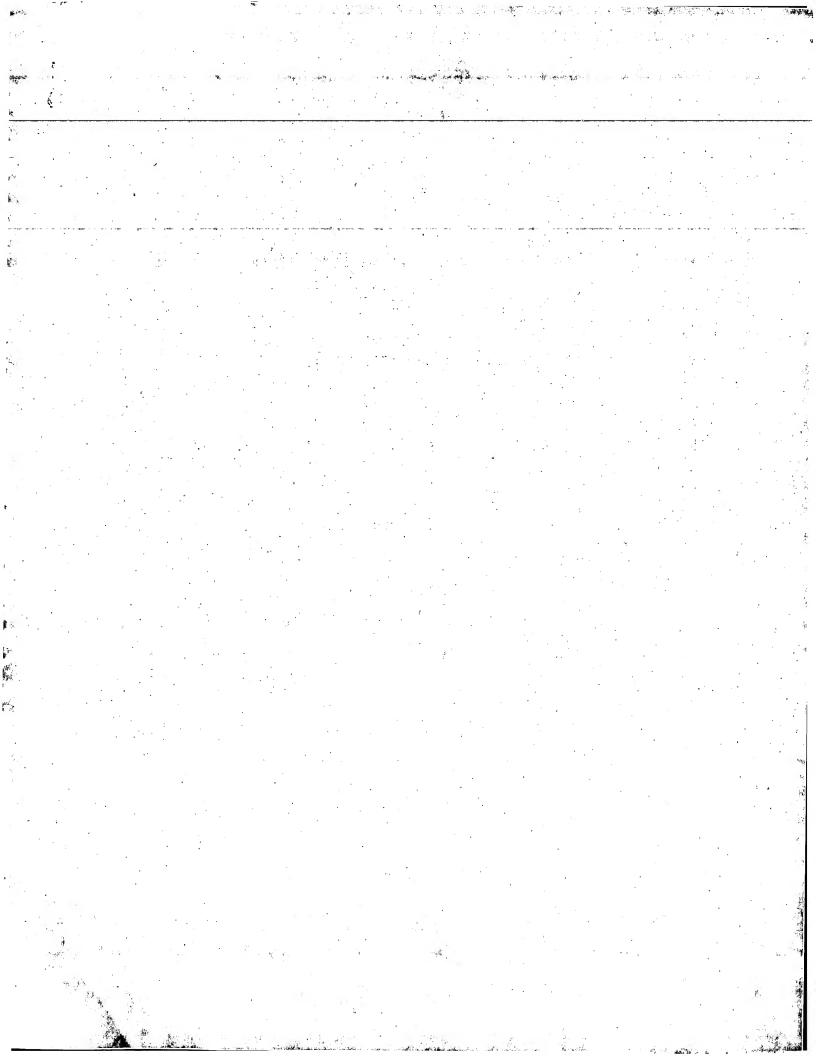
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RESULT 15
AAZ27914
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Best Local
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AAZ27913/c
ID AAZ27913 standard;
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AAZ27914 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 79. 
Matches 23; Conservative
                                                                                                                                                                                             The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules e.g. an encoded proteins can be used for preventing or treating diseases, development, graft rejection, inflammation, infectious diseases, tumor such as atopic dermatitis. They can be used in mammals such humans, dogs, cattle, sheep or pets. The products can also be used for detection, diseases.
                                                                                                                                                                 Sequence 1897 BP; 585 A; 400 C; 383
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 97-99; 148pp; English.
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17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                     treating,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B7; CTLA4; T cell costimulatory protein; allergic reaction; infectious disease; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               graft rejection;
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                                                             906 GTACTCTTTCCTTGGTCTGCTCACTTTCT
                                                                            2 GGACTCAGTCCTTGGTCATCTCACCTTCT
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                                                                                                                      23;
                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                 e.g. autoimmune and atopic diseases
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                                                                                                                  Conservative
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98US-0062597
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 DNA; 1897
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79.38;
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Pred. No. 65;
0; Mismatches
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Mismatches
                                                                                                                                                              G; 529 T; 0 other;
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(first entry)

AAZ27914;

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Search completed: July 10, 2003, 19:52:36 Job time: 66.3034 secs
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                                                                                                                                                                            Query Match 64.7%;
Best Local Similarity 79.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                      The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                               Sequence 1897 BP; 529 A; 383 C; 400 G; 585 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine B7-2 gene complementary DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 101-102; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-571822/48.
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17-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases. -
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                                                                                       98US-0078765.
98US-0062597.
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Maximum DB seq length: 2000000000
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56.0	56.7	56.7	56.7	57.3	57.3	57.3	57.3	57:3	58.0	58.0	58.0	58.0	58.7	58.7	58.7	58.7	58.7	
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Sequence 32, Appl.	Sequence 4, Appli	Sequence 4, Appli .	Sequence 4, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 84, Appl	Sequence 84, Appl	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5212286	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	
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Sequence 1. 2 57.3 376 1 US-08-162-809-7 Sequence 1. 2 57.3 376 1 US-08-162-809-7 Sequence 2. 2 57.3 6585 3 US-08-746-111-4 Sequence 4. 2 57.3 6585 3 US-08-746-111-4 Sequence 4. 2 57.3 6585 3 US-08-746-113-4 Sequence 4. 2 57.3 6585 3 US-08-746-113-4 Sequence 4. 2 57.3 6585 3 US-08-746-113-4 Sequence 4. 2 58.7 999 2 US-08-394-4428-4 Sequence 4. 2 58.0 426 4 US-09-712-016-32 Sequence 3.	4 58.0 4149 2 US-08-737-715-1 Sequence 1, 35081 2 US-08-752-760A-1 Sequence 2, 57.3 330 1 US-08-081-539-84 Sequence 84, 2 57.3 330 1 US-08-66-647-84 Sequence 84, 2 57.3 3374 PGT-US96-03965-1 Sequence 1, 2 57.3 3776 1 US-08-162-809-7 Sequence 7, 2 57.3 6585 3 US-08-746-111-4 Sequence 4, 2 57.3 56.7 999 1 US-08-44-9888-4 Sequence 4, 2 56.7 999 2 US-08-34-4428-4 Sequence 4, 2 56.7 999 2 US-08-34-4428-4 Sequence 4, 2 56.0 426 4 US-09-712-016-32 Sequence 32,	17.4 58.0 2589 6 5212286-1 17.4 58.0 4149 2 US-08-737-715-1 17.4 58.0 35081 2 US-08-737-715-1 17.4 58.0 35081 2 US-08-752-760A-1 17.2 57.3 330 1 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US-09-712-016-32	17.6 58.7 5470 2 US-08-443-861-1 Sequence 1, 58.7 5470 4 US-08-13-829B-1 Sequence 1, 17.6 58.7 43804 4 US-09-171-61-1 Sequence 1, 17.4 58.0 2533 4 US-09-171-61-1 Sequence 1, 17.4 58.0 2533 4 US-09-149-922-5 Patent No. 5: 58.0 2589 6 5212286-1 Patent No. 5: 58.0 2589 6 5212286-1 Sequence 1, 17.4 58.0 35081 2 US-08-737-715-1 Sequence 1, 17.4 58.0 35081 2 US-08-752-760A-1 Sequence 1, 17.2 57.3 330 1 US-08-61-339-84 Sequence 1, 17.2 57.3 330 1 US-08-466-647-84 Sequence 1, 17.2 57.3 330 1 US-08-466-69-7 Sequence 1, 17.2 57.3 37.76 1 US-08-162-809-7 Sequence 1, 17.2 57.3 6585 3 US-08-746-111-4 Sequence 4, 17.5 5.7 999 1 US-08-16-478A-4 Sequence 4, 17.5 5.7 999 2 US-08-416-478A-4 Sequence 4, 17.5 5.7 999 2 US-08-394-442B-4 Sequence 3, 18.8 56.0 426 4 US-09-712-016-32 Sequence 3, 20-08-394-442B-4	17.6 58.7 5406 5 PCT-US92-00893-5 Sequence 5, 58.7 5470 2 US-08-443-861-1 Sequence 1, 17.6 58.7 5470 4 US-08-193-829B-1 Sequence 1, 17.6 58.7 5470 4 US-08-193-829B-1 Sequence 1, 17.6 58.7 43804 4 US-09-171-461-1 Sequence 1, 17.4 58.0 2533 4 US-09-149-922-5 Patent NO. 55. 17.4 58.0 2533 4 US-08-737-715-1 Sequence 5, 17.4 58.0 2589 6 5212286-1 Sequence 1, 17.4 58.0 35081 2 US-08-737-715-1 Sequence 1, 17.4 58.0 35081 2 US-08-737-700A-1 Sequence 1, 17.2 57.3 330 1 US-08-466-647-84 Sequence 8, 17.2 57.3 330 1 US-08-162-809-7 Sequence 1, 17.2 57.3 37.6 1 US-08-162-809-7 Sequence 4, 17.2 57.3 6585 3 US-08-746-111-4 Sequence 4, 17.2 57.3 6585 3 US-08-416-478A-4 Sequence 4, 17.5 5.7 999 2 US-08-416-478A-4 Sequence 4, 17.5 5.7 999 2 US-08-344-42B-4 Sequence 3, 17.5 5.0 999 2 US-08-344-42B-4 Sequence 3, 18.8 56.0 426 4 US-09-712-016-32 Sequence 3, 25.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0	17.6 58.7 5406 5 PCT-US92-05401-5 Sequence 5, 58.7 5470 2 US-08-443-861-1 Sequence 1, 17.6 58.7 5470 4 US-08-13-829B-1 Sequence 1, 17.6 58.7 5470 4 US-08-13-829B-1 Sequence 1, 17.6 58.7 5470 4 US-08-13-829B-1 Sequence 1, 17.6 58.7 5470 4 US-09-171-461-1 Sequence 1, 17.4 58.0 2533 4 US-09-171-461-1 Sequence 5, 17.4 58.0 2533 4 US-08-737-715-1 Sequence 5, 17.4 58.0 2589 6 5212286-1 Sequence 1, 17.4 58.0 35081 2 US-08-737-715-1 Sequence 1, 17.4 58.0 35081 2 US-08-737-700A-1 Sequence 1, 17.2 57.3 330 1 US-08-081-539-84 Sequence 8, 17.2 57.3 330 1 US-08-16-809-7 Sequence 1, 17.2 57.3 37.4 Sequence 1, 17.2 57.3 6585 3 US-08-16-809-7 Sequence 4, 17.2 57.3 6585 3 US-08-16-809-7 Sequence 4, 17.2 57.3 6585 3 US-08-34-11-4 Sequence 4, 17.5 5.7 999 1 US-08-416-478A-4 Sequence 4, 17.5 5.7 999 2 US-08-34-442B-4 Sequence 3, 18.8 56.0 426 4 US-09-712-016-32 Sequence 3, 18.8 56.0 426 4 US-

## ALIGNMENTS

Patent No.

Application US/08299682

GENERAL INFORMATION:

TITLE OF INVENTION: MG
TITLE OF INVENTION: F]
NUMBER OF SEQUENCES: ]
CORRESPONDENCE ADDRESS:

Watson,

Mary Ellen

Robert Malcom Methods for In-Solution Quenching of

Fluorescently Labeled Oligonucleotide Probes

ADDRESSEE:

Hoffmann-La

Roche

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                                                                                                               ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-299-682-13
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                        Best Loc
Matches
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                       STRANDEDNESS:
                                                                      Local
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                        l Similarity
30; Conserv
             1.TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
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                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 Kingsland Street
                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                             DNA (genomic)
                                                                                                                                                        single
                                                                    63.3%;
96.8%;
                                                                                                                                                                                                                                                                                                                                                                 US/08/299,682
                                                       Score 19; DB Pred. No. 9.2; 0; Mismatches
                                                          0,
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                                                                                    Length 33;
                                                          Indels
                                                        1;
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equence 1;
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OPERATING SYSTEM:
                  MPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Petry, Douglas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (510) 814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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NEW JERSEY
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                                                                                                                                                                                                                                                                                                    TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA:
                                                                                                                                                                                                                               Application US/08705771
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA (genomic)
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                                                                                          6 BECKER FARM ROAD
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                                                            USA
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              IBM PS/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (510)
                                                                                                    CARELLA, BYRNE, BAIN, GILI
CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoffmann-La
                                                                                                                                                                                   Moore, Reiner Gentz, Hongjin Ji,
                                                                                                                                                                                                                                                                                                                                                                                                                           single
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MS-DOS
                                                                                                                                                               and Jing-Shan Hu
Human Genes, Sequences and
                                                                                                                                                   Expression Products
                                                                                                                                                                                                                                                                                                                                                      96.88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roche Inc.
                                                                                                                                                                                                                                                                                                                                                   Score 19; [
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                GILFILLAN,
                                                                                                                                                                                                                                                                                                                                                           Length 33;
                                                                                                                                                                                                                                                                                                                              Gaps
                                         Patent No.
                                                                                                                                                                         Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Sequence 3, Application US/09081689
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NUMBER OF SEQUENCES.

NUMBER OF SEQUENCES.

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

Floppy disk

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 786 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
IRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 550 base pairs
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                                                                                                                                                                                                                                              205 GACCCCCTCCTTGGTCTTCTCAGCTGCT 178
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                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GACCCCCTCCTTGGTCTTCTCAGCTGCT 95
                                                                                                                                                                                                                                                                                                        3 GACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GACTCAGTCCTTGGTCATCTCACCTTCT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Wallis, Nicola G.
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: PCT/US95/08295
30-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  August 30, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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78.68;
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Pred. No. 2
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                26;
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Zalacain, Madgalenaa Throup, John Biswas, Sanjoy

ORRESPONDENCE ADDRESS: TITLE OF INVENTION:

Histidine Kinase

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US-08-858-207A-66/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                 ORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                           SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILING DATE: 30-MAY-1997
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                  TLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                             OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                                                  CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
FILING DATE:
                APPLICATION NUMBER:
                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Falk, Stephen T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/081,689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   792 GTCCTCGGTCATCTCACCTT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          INFORMA
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                                                                                                                         19406-0939
                                                                                                                                                                                                                                                                                                                                                         b, Application US/08858207A
6348328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                       USA
                                                                                                                                                                                                                                Stodola, Robert
VENTION: No. 6348328el Compounds
EQUENCES: 552
                                                                                                                                                                                                                                                                           Hodgson, John
Knowles, David
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215-994-2222
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                                                                        IBM Compatible
09-MAY-1997
                                                                                                                                                                                                                                                                                                                         Michael
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                                         DOS
for Windows Version 2.0
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            US/08/858,207A
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Pred. No. 2
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GENERAL INFORMATION:

APPLICANT:

FILE REFERENCE: 1340-1-016
CURRENT APPLICATION NUMBER: US/09/073,541A
CURRENT FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 46

APPLICANT: TOUMANEN, Elaine TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME FILE REFERENCE: 1340-1-016

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                                            RESULT 8
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                          US-09-073-541A-13/c
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                                                                                                                                                                                                                                                                  SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Sequence 13, Application US/09073541A Patent No. 6448224
                                                                                                                                                Matches
                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/305,984B
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,399
EARLIER FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 09/
EARLIER FILING DATE: 1999-05-05
                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 1340-1-016N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERAL INFORMATION:
                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                   LENGTH: 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                              PLICANT: Toumanen, Elaine
TLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  792 GTCCTCGGTCATCTCACCTT 773
                                                                                      264 GTCCTCGGTCATCTCACCTT 245
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                                                                                                                   GTCCTTGGTCATCTCACCTT 28
                                                                                                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 6331407ak,
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95.0%;
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Pred. No. 2
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Pred. No. 2
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ENGTH:

PatentIn Ver.

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Query Match |
Best Local Similarity
Matches 19; | Conserve
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US-09-081-689-1
                                                      Matches
                                                                                Query Match
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                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1526 base pairs
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,347.
ETLING DATE: 30-MAY-1997.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM
ELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0b RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                     Local
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461 GTCCTCGGTCATCTCACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19103-2793
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              philadelphia .
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                        GTCCTTGGTCATCTCACCTT 28
                                                                                                                                                          nucleic acid
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4000 Bell Atlantic Tower, 1717 Arch Stre
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Biswas, Sanjoy |
PENTION: Histidine Kinase
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                                                        Conservative
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                                                                                                                                           double.
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Pred. No. 28;
0; Mismatches
                                                                     Score 18.4;
Pred. No. 2
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   442
                                                           Mismatches
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RESULT 10 US-08-751-189

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US-09-060-836-1
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Patent No. 59817
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NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein TITLE OF INVENTION: 1
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC.compatible
COMPUTER: IBM PC.compatible
COMPUTER: DC.COMPUTER: COMPUTER: COMPUTER
COMPUTER: COMPUTER
                              SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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LE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein
LE OF INVENTION: 1
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                                                                                                                                                                                                                                                                                                                                                                                               STREET:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                    E: Amgen, Inc.
1840 De Havilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7881 base pairs
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78.6%;
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                                                            Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,688
US/09/060,836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.4;
Pred. No. 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US 08/751,189

15-NOV-199

REGISTRATION NUMBER:

Oleski,

Nancy A.

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                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: US-09-184-445-1
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                              Matches
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
COUNTRY:
ZIP: 91320-1785
ZIP: 91320-1785
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Oleski, Nancy A. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICATION NUMBER: US UN PPLICATION NUMBER: US UN PPLICATION DATE: 15-NOV-1996
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5358 GGACACAGTCCGTGGGCAGCTGGCCTTC 5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION DATA:
                                     2 GGACTCAGTCCTTGGTCATCTCACCTTC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thousand Oaks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7881 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7881 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harrington, Lea A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                            61.3%;
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                                                                                                                                                                            Score 18.4;
Pred. No. 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                          Mismatches
                                                                                                                                                                                                              DB
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                                                                                                                                          6;
                                                                                                                                                                                                              Length 7881;
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                                                                                                                                          Indels
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                                                                                                              RESULT 15
US-08-961-527-140
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US-09-073-541A-25/c
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                                                                                                                                                                                                                                                                                                                             US-09-073-541A-25
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LENGTH: 8900
                                                                                                                                                                                                                                                           Matches
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                                                                                   Patent No.
                                                                                                   Sequence 140, Application US/08961527
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09073541A Patent No. 6448224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 46
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NUMBER OF SEQ ID NOS: 7.6
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EARLIER APPLICATION NUMBER: 60/084,399
EARLIER FILING DATE: 1998-05-06
                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/073,541A
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                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Toumanen, Elaine
ITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 8900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LE REFERENCE: 1340-1-016N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICANT: Toumanen, Elaine
TLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
CORRESPONDENCE ADDRESS:
                NUMBER OF SEQUENCES:
                                   TITLE OF INVENTION:
                                                 APPLICANT:
                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ER APPLICATION NUMBER: 09/305,984
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b. 6331407
                                                                                                                                                                                                         9 GTCCTTGGTCATCTCACCTT 28
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                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 6448224ak, Rodger
                                                 Charles Kunsch
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                       95.0%;
                                Streptococcus pneumoniae Polynucleotides and Sequences
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                                                                                                                                                                                                                                                         0
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Pred. No. 3
                                                                                                                                                                                                                                                                           Score 18.4;
Pred. No. 3
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Bd
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                                                                                                                                                                                                                                                                                       Length 8900;
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Human Genome Sciences, 9410 Key West Avenue

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APPLICATION:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 140:
SEQUIENCE CHARACTERISTICS:
LENGTH: 28882 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
Search completed: July 10, 2003, 20:27:14
Job time: 15.4157 secs
                                                                                                                                               Query Match 61.3%;
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: HE COMPUTER: HE COMPUTER: HE SYSTEM: MSLUS
SPETWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                            2314 GTCCTCGGTCATCTCACCTT 2333
                                                                                                              9 GTCCTTGGTCATCTCACCTT<sub>1</sub> 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Diskette, 3.50 inch, 1.4Mb storage
HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                         PB340P1
                                                                                                                                                    Score 18.4; I
Pred. No. 42;
0; Mismatches
                                                                                                                                                                                 DB 4; Length 28882;
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                                                                                                                                                        0;
                                                                                                                                                        Gaps
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: Sequence: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Database : Total number of hits satisfying chosen parameters: Searched: Run on: OM nucleic - nucleic search, using sw model Scoring table: July 10, 2003, 18:15:27; Search time 285.951 Seconds (without alignments) 3358.597 Million cell updates/sec Gapop 10.0 , Gapext 1.0 US-10-087-631B-5 33 2054640 seqs, 14551402878 residues 1 gccacatgagtggcaaggcgtctggtgataccg gb\_ba: em\_htgo\_hum:\*
em\_htgo\_mus:\*
em\_htgo\_other:\* em\_htg\_mus:\*
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em\_htg\_inv:\*
em\_htg\_other:\* 33 4109280

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

REFERENCE AUTHORS	SOURCE	ACCESSION VERSION	DEFINITION	LOCUS	RESULT	•	45	C 43	c 42	41	39	38	ω	ດ ມູນ 4	C 33,	c 31	30	งง	c 27	งผ	N	. c 222	N	ں ب		دم د	c 14	<b></b>	c 11	_	ာ ထာ -	7 0	ν Ω.	م	2 02 H	NO.	Result
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rimates; Catarrhini	a; Craniata;	2	om clone 125N5	84126 bp DNA		ALIGNMENTS	AC099284	AC12468/ AC099383	AL772301	AC015911	AC078784	AC103385	AC110331	AC068576	AC022794	AC101633 AC022794	AC101633	HSDJ60019	AC129879	AC118767 AC025397	HEC295172	E30279192 AF179613	E30279191	E30279196	AE003418	AC021368	AC104502 . AC087522	AL133294	AC087531	DMC118B3	20	AC109903 ·	AC104398	RNO251687	HS125N5 AL136099	;	
ae; Homo.	Vertebrata; Euteleostomi;		omosome 6q26-27. Contain	linear PRI 23-NOV-1999		-	99284 Rattus	ACIZ468/ MUS muscu	Mus mus	Homo sap	4 Homo	AC103385 Mus muscu	1 Rattus	~ ·	94 Hom		Sum S	Human [	Rattus	Rattus	ผ	Echov i	AJ279191 Echovirus	5 8	AE003418 Drosophil		AC104602 Drosophii AC087522 Homo sapi	Humar	-	Drosophi	AC102955 Rattus no	AC109903 Rattus no	8 Rattus n	J251687 Ra	man [	iption	

IS125N5	
	HS125N5 84126 bp DNA linear PRI 23-NOV-1999
DEFINITION	Human DNA sequence from clone 125N5 on chromosome 6q26-27. Contains
	a putative novel gene, ESTs, STSs and GSSs; complete sequence.
CCESSION	AL008728
ERSION	AL008728.1 GI:3820992
(EYWORDS	HTG.
SOURCE	Homo, sapiens.
ORGANISM	Homo sapiens .
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
•	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 84126)
AUTHORS	Mashreghi-Mohammadi, M.
TITLE	Direct Submission

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	/note="36 copies 2 mer aa 68% conserved"		.10330 - "L1PB1 repeat: matches 52216118	<pre>/note="HEXYH, repeat: matches 2669284/ of consensus" 92939405 /note="MEEGAD repeat: matches 1114 of consensus"</pre>	HERVH repeat: matches 31863637 of		8254 . 8491 /note="HERRYH repeat: matches 4314 . 4531 of consensus" 8575 8676	1.	epeat: matches 554689.of	.5306	.5072 ="MIR repeat:	ement(40974389) ="match: GSS AQ053978"	26842794 / /note="AluSg/x repeat: matches 178288 of consensus"	/note="match: EST AA732827" /note=mentch: experimental	1 (BITTATIVE DOVAL)	"dJ125N5.1"	opies	١.	68374 /note-"AluSx repeat: matches 1303 of consensus"	/map= '420'-2/; /clone="RRP1-125N5" /clone_11b-"RPCI-1"	/db_xref="taxon:9606" /chromosome="6"	organism="Homo sapiens"	see http://bacpac.med.buffalo.edu/ Location/Qualifiers	s from the library RPCI1 constructed at the Institute by the group of Pieter de Jong. For	urther information can be found at r.ac.uk/HGP/Chr6	some 6, constructed by the Sanger Centre Chromosome (	sequence is ambiguous, there is an annotation using the 'unsure' feature key	sive air sequencing problems, sis, but not necessarily within	n finished according to sequence map criteria as follows.	as described above. entire insert of clone 125N5. This sequence	be found in the sequence	lifferences are found these are annotated as variations with a note of the overlapping clone name. Note the	seq	ed (04-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, 35, UK. E-mail enquiries: humquery@sanger.ac.uk Clone	
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                                                                                                                                                                                                                                                                                                    156998 bp DNA
Homo sapiens chromosome 6 clone RP11-270C4,
PROGRESS ***, in unordered stoom
Center: Sanger Centre
Center code: SC
                                                 On Aug 11, 2000 this sequence version replaced gi:9588114
                                                                                     Submitted (13-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10.1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                Homo sapiens
                                                                    requests: clonerequest@sanger.ac.uk
                                                                                                                          Direct Submission
                                                                                                                                            Phillimore, B.
                                                                                                                                                       Mammalia; Eutheria; Pr
1 (bases 1 to 156998)
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30062. .30361
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complement(43225. .43547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="23 copies 36 mer 63% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                      GI:9796029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e="277 copies 3 mer tga 63% conserved"
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83.9%;
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                           Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delando, C., Denn, A.L., Ding, Y., Dinh, H.H., Delanday, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Frants, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 155262 bases at least Q40 Consensus quality: 155772 bases at least Q30 Consensus quality: 155890 bases at least Q20
   Gabisi, A.,
                                                                                                                                                                                                                          Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopou Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R.,
                                                                                                                                                                                                                                                                                                                                                                              Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarla, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC096936 178874 bp Rattus norvegicus clone CH230-41H3,
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                                                                                                                                                                                                                                                                                                    Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                                                                                                                                                                                                           Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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Insert size: 157873; 2.1% error; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA270C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence
This record will be available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCACATGAGTGGCAAGGCGTCTGGTGATAC 31
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/db_xref="taxon:9606"
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Gao, J., Garcia, A.,
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Pred: No.
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Garner, T.,
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                                                                                                                                                                                                                                                                 Christopoulos, C
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   Garza, N.,
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                                          Frantz, P.,
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Maheshwari, M

Li, J., Li, Z., Kratovic,

.ozado,R.J., Lu,

Jacobson, B., Jia, Y. Karlsson, E., Kelly,

length

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pirect Submission
Submitted (03-007-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 178874)
Worley, K.C.
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 12, 2002 this sequence version replaced g1:17973294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, G., Williamson, A., Wiec
Wu, C., Wu, Y., Wu, Y.F., Zhou, J.,
Weinstock, G. and Gibbs, R.
Direct Submission
                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | (bases 1 to 178874)
| Worley, K.C.
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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peerry,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Roife,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
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Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
                                                                                                                                                                                                                                                                                                           Squencing vector: Plasmid;
Chemistry: Dye-terminator Blg Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113609 bases at least 040
Consensus quality: 119045 bases at least 030
Consensus quality: 124009 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: GHQD
Center clone name: CH230-41H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web'site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine Center code: BCM
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1168: contig
1268: gap of
2835: contig
2935: gap of
4058: contig
4158: gap of
5514: contig
5614: gap of
                                                                                                                                           t the exact sizes of the gaps are unknown.
ill be updated with the finished sequence
is available and the accession number will
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Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
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                            g of 1168 bp in 1
f unknown length
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g unknown length
g of 1123 bp in 1
f unknown length
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Organ,M., Morris,S.,
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                                                                                                                                                                                                                               MOTIVANNA, A. and Yonezawa, S.

MOTIVANNA, A. and Yonezawa, S.

Molecular cloning of neonate/infant-specific pepsinogens from rat
stomach mucosa and their expressional change during development
stomach Blophys. Res. Commun. 267 (3), 806-812 (2000)
                                                                                                                              Modeling Research, Primate Research Institute, Inuyama, 484-8506, JAPAN
                                                                                                                                                            Direct Submission
Submitted (25-NOV-1999) Kageyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                           pepsinogen F protein.
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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
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                                                                                                                                                                                         Kageyama,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity .
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jeyama,T., Ichinose,M.,
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78684
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                                                              /db_xref="taxon:10116"
/clone="pRT723"
                                                                                                 /organism="Rattus norvegicus"
                                                                                                              Location/Qualifiers
l. .1333
                         /function="unknown"
                                               /dev_stage="4-day-old infant"
                                                                                      /strain="SD"
'product="pepsinogen F protein"
              codon_start=1/
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of 3750
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of 2998
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mat_peptide
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Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Elagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hennandez, O., Hodgson, A., Hogues, M., Juwes, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kureshi, A., 'Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Kratovic, J., Kureshi, A., 'Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N.,
Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N.,
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Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Ortedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus, E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C. Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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/translation="MKHLWULGIVALSECLVKIPLMKIKSMRENLRESHMLKDYLEKY
PRSRAHVLLEQRRNPSYTYEPMRNYLDLVYIGTISIGTPPQEFKVVLDTGSSDLWVPS
IYCSSPACAHKKVFNPLQSSTFLVSGRPVNVAYGSGEMSGFLAYDTVKIGDLTVVAQA
FGLSLEEPGRFMEHAVFDGILGIGYPNLGLQGVTPVFDNLWIQGLIPQNLFAFYLSSK
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78.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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; Murinae;
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IN PROGRESS
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*		of 1340 l unknown : of 1318 l unknown l of 1533 k	8714: contig 8714: gap of 10066: contig 10166: gap of	0: gap of 8: contig 8: gap of	3533: contig of 1309 page 3533: gap of unknown 4846: contig of 1213 page 6 unknown 5170.	1 1024: contig of 125 1124: gap of un 25 2124: contig of 25 2224: gap of un	l be update s available	of N, but the exact sizes of the case are	differ from s du/docs/Genba sequence. It	Sensus quality: 125749 bases at	g vector: plasmid; : Dye-terminator Big Dye: 100% program: Phrap; version 0.99032 quality: 115292 bases at least	Center project information Center clone name: GIQD Center clone name: CH230-128124	code: Book Book Book Book Book Book Book Boo	11, 2002 this seter: Baylor Col	Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77040 medicine, One		Submitted (09-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 Issa	2 (bases 1 to 187614) Worley, K.C. Direct Submission	a,S.,,Nelso	Wand, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Mooré, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Worley, K., Wu, Y.; Zhang, T., Wang, C., Wu, Y.; Wu, Y.; Zhang, T., Wang, C., Wu, Y.; Wu, Y.; Zhang, T., Wang, C., Wu, Y.; Wu, Y.; Zhang, T., Wang, C., Worley, K., Worley, W., Wang, C.,
82045: gap of	78203: gap of unknown length 78867: contig of 2664 bp in 78967: gap of unknown length 80169: contig of 1202 bp in 80269: gap of unknown length 81945: contig of 1672 h	* 68895 71194: contig of 2300 bp in length * 71195 71294: gap of unknown length * 71295 73669: contig of 2375 bp in length * 73670 73769: gap of unknown length * 73770 76103: contig of 2334 bp in length	66619: contig of 2087 bp i 66719: gap of unknown leng 68794: contig of 2075 bp i 68894: aga of unknown leng	62993: contig of 1918 bp in 63093: gap of unknown lengt 64432: contig of 1339 bp in 64532: gap of unknown lengt	59031: contig of 2210 l 59131: gap of unknown l 60975: contig of 1844 l 61075: gap of unknown l	55387: Conting of 1740 bp i 55487: gap of unknown leng 56721: conting of 1234 bp i 56821: gap of unknown leng	50378: gap of unknown 53547: contig of 3169 53647: gap of unknown	46195: gap of unknown length 48271: contig of 2076 bp in 48371: gap of unknown length	44509: contig	42091: gap of unknown lest 43128: contig of 1037 bp 43228: gap of unknown lest	3949: contig of 1124 bp in 39589: gap of unknown length 40625: contig of 1036 bp in 40725: gap of unknown length 41991: contig of 1266 bp in	37075: gap of 38265: contig 38365: gap of	3503: gap of unknown length 3503: contig of 1390 bp in 35793: gap of unknown length 36975: contig of 1182 bp in	32329: contig 32329: gap of 34203: contig	2930/: gap of unknown length 30996: contig of 1689 bp in 31096: gap of unknown length	27584: gap of 29207: contig	24330: gap of unknown length 26274: contig of 1724 bp in 26374: gap of unknown length	23101: contig of 1264 bp i 23101: gap of unknown leng 24450: contig of 1349 bp i	20475: gap of unknown length 21637: contig of 1162 bp in 21737: gap of unknown length	19236: gap of u 20375: contig o

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Matches 25
TITLE
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                                                                                    Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.,
Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Miner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Primus, E., Pu, L., Ouiles, M., Ren, Y.,
Peters, L., Pickens, R., Primus, E., Pu, L., Ouiles, M., Ren, Y.,
Soherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, P., Telfrod, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Wallamson, A., Wleczyk, R., Woden, S., Wotley, K.,
Wu, Y., Zhou, J., Zorrilla, S., Welson, D.,
Welson, D., Welson, D., Pelson, D.,
Welson, D., Welson, D., Welson, D., Welson, D.,
Welson, D., Welson, D., Welson, D., Welson, D.,
Welson, D., Welson, D., Welson, D., Welson, D.,
Welson, D., Welson, D., Welson, D., Welson, D.,
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AC1191
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Rattus norvegicus clone CH230-375H21,
***, 62 unordered pieces.
AC11975
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Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Ealls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Fran
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                                                 Wu,C., Wu,Y., Wu,Y.F., Zh
Weinstock,G. and Gibbs,R.
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
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                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bouck, J., Bowie, S., Brieva, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus.
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87042:
                                                                       Wu, Y.F., Zhou, J.,
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Burkett, C., Burrell, K.L., Byrd
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tunge,H.C., Are,J.R., Ayele,M.,
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                                                                            Zorrilla, S.,
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IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-APR-2002) Human Genome Sec
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces
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Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                       Worley, K.C.
Direct Submission
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                                                                                                                                    Direct Submission
                                                                                                                                             Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Weinstock,G. and Gibbs,R.
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Bryant, N.P. Banks,T.,

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COMMENT

AUTHORS TITLE JOURNAL

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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Jul 12, 2002 this sequence version replaced gi:18860273.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
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Assembly program: Phrap; version 0.990329
Consensus quality: 150710 bases at least Q40
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Maheshwari, M., Mapua, P., Martindale, A., Morris, S., Morris, S., Morris, S., Morris, S., Morris, A., Novembur, G., Morris, S., Martindale, A., Martindale, A., Martindale, A., Martindale, A., Tang, H., Stone, H., Taylor, T., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Talfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Marren, B., Ward-Moore, S., Marren, B., Ward-Moore, S., Marren, B., Ward-Moore, S., Marren, B., Wang, Q., W
                                                             Submitted (11-JUL-2002) Human Genome Sequencing Center, Deparate Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced oi:17947947
                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
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Direct Submission
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Barbaria,J., Benton,J., Bimage,K.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently consists of 167 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                            as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: Assembly program: Phrap; version 0. Consensus quality: 163376 bases at Consensus quality: 175615 bases at Consensus quality: 184652 bases at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name:
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D89010.1
Department of Anatomy and Physiology, Medical Sciences Institute, University of Dundee, Dundee DD1 4HN, U.K.

2 (bases 1 to 24263)
                                                                                                                                                                                                                            Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster
AL031582 GI:4176433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamada, O.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus oryzae
Eukaryota; Fungi;
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                                                                                                Unpublished
                                                                                                                               Sequencing the distal X chromosome of Drosophila melanogaster
                                                                                                                                                              Philippe, Valenti., David, Glover.
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IMPORTANT: This sequence is NOT necessarily the entire insert of clone 118B3. It may be shorter, since we are minimising the overlap between clones to 100 bases, by trimming them. Clone 118B3 overlaps to the left with clone 11F6

The true left end of clone 118B3 is at position 34769 of clone 11F6 Clone 118B3 overlaps to the right with clone 115C2 The true right end of clone 118B3 is at position 385 of clone 115C2 Sequence in absolute orientation with respect to chromosome Clone=118B3; Contig ID=14; Length=2463; Status=Finished The syntax for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consortium
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ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.
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aall: benos@eb1.ac.uk on behalf of the European Drosophila Genome
quencing Consortium. For further information see the European
sophila Genome Sequencing Consortium's web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //edgp.ebi.ac.uk/
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method:''blastx'', version:'/1.4.9'')
/match-(desd:''GH04661.5prime GH Drosophila melanogaster bead p072 Drosophila melanogaster cDNA clone GH04661
Sprime, mRNA sequence'', species:'Drosophila melanogaster
                                                                                               (fruit fly)", ranges:(query:22139...22499, target:EMBL::A1064293.361...1, score: '1796.00")), method: 'blastn', version: '1.4.9")
/match-(desc: 'GH05563.5prime GH Drosophila melanogaster head por 2 Drosophila melanogaster: 'DNA clone GH05563
5prime, mRNA sequence', species: 'Drosophila melanogaster (fruit fly)", ranges:(query:21611...21808)
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ranges:(query:13748. .13954,
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method:''blastx'', version:''1.4.9'')
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/prediction=(method:'/genscan'', version:''1.0'')
/match=(desc:''KIAA0376 PROTEIN (FRAGMENT)'',
                         (fruit fly)'', ranges:(query:21611. .21808, target:EMBL::AI107734:198. .1, score:''972.00''.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                species: ''HOMO SAPIENS (HUMAN)
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5. .14746,14809. .16087,16160. .16336,16886.
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0.00'')),
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                                                              score: ''972.00''),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'ConnorT, O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
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Camarata, J., Campopiano, A., Choepel, Y.,
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wurphy,T., Naylor,J., Nguy
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                                                                                                                                                                                                                                                                                                   will be sequenced
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7763 c 7710 g 9183 t 6427 ot
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/db_xref="taxon:9606"
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19835: gap of 122
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35145: contig of 561 bp
5245: gap of 100 bp
35799: contig of 554 bp
5899: gap of 100 bp
36445: contig of 546 bp
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82: contig of 553 bp in length
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Pred. No. 2.1e+02;
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Muscomorpha;
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FEATURES
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sections only once, except for a 100 base overlap. The true left end of clone RP5-1135K18 is at 1 in this The true left end of clone RP5-1169J3 is at 106166 in

in this sequence.

Location/Qualifiers

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COMMENT
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TITLE
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Best Local Similarity 75.8%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91773 GTCGGAGGAGTGGTACGGCGTCTGGGGATCCCG
IMPORTANT: This sequence is not the entire insert of clone RP5-1135K18 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP5-1135K18 is at 1 in this sequence.
                                                                                                                                                                                                                       The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                               This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                             from the library RPCI-5 constructed institute by the group of Pieter de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                       nttp://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       only a small overlap as described above.
This sequence has been finished according
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to the overlapping clone, as we submit sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AL133294
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Human DNA sequence from clone RP5
Contains GSSs, complete sequence.
AL133204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-DEC-1999) Celera Genomics, 45
Rockville, MD, USA
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                                                                                                                                             /www.sanger.ac.uk/Projects/C elegans/wormpep RP5-1135K18 is the library RPCI-5 constructed at the Roswell park Cancer the by the group of Pieter de Jong. For further details see
                                                                                                                  PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000 this sequence version replaced gi:9501134.
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23342 c 23493 g 27708
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db_xref="taxon:7227"
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e RP5-1135K18 on chromosome 11p12-14.1
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<pre>misc_feature misc_feature</pre>		misc_feature	1 1	repeat_region	- 1	repeat_region	repeat_region	repeat_region		misc_feature	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		repeat_region		- 0	misc_feature	repeat_region	repeat_region	repeat_region	۲.	repeat_region		source
3345. 13683) : GSS: Em:AQ091582* 3384. 13771) : GSS: Em:AQ005856*	S: Em:AQ432970"	ement(1334813905)  ""match: GSS: Em:B05804"  ement(1330013785)	-"AluJb repeat12743	11859. 12150 /note="AluSx repeat: matches 1295 of consensus" 12175. 12366	-"LIMC5 repeat: matches 77057917	/note="AluSq repeat: matches 1308 of consensus" 1125111515 /note="17 repeat: matches 7/51 27/0 of consensus"	"MIR repeat: matches 149207	/note="match: GSS: Em:AQ386199" 1079610853		ement(10129 .10648) ="match: GSS: Em:AQ771611"	/note="MIR repeat: matches 49262 of consensus" 996710097 /note="Allulb repeat: matches 398 of consensus"	"AluSx repeat: matches 1312 of .9676	90419004 /note="12 copies 2 mer tt 81% conserved" 9087. 9396	= "L1MEc repeat: matches 22572378	/HOLE- LIMEC Lebeal: Halches 23//21// OI CONSENSE: 84208724 /HOLE- #Allis repeat: matches 1 298 of consense:	"Alusx repeat: matches 1303 of cons	e="IlMEc repeat: matches 21772 8277	/note="MIR repeat: matches 6262 of consensus" 77467969	/note="MIR repeat: matches 48 .261 of consensus"  Alto 6734	33493 h: GSS:	.3363 -"match: GSS: Em:B01382"	3094 "L2 repeat: matches 2426.	t: matches 5927613	42 copies 2 mer tt /1% conserved"	"AluSx repeat: matches 1	11b="RP	/chromosome="11" /map="p12-14.1" /clone="RP5-1135K18"	1106265 /organism="Homo sapiens" /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92630 GCCACAGGAGGGCAGGGAGGTTGGTGATCCAG 92598
                                                                                                                                                                                                                                                                                                        Worley,K.C.

Direct Submission

Submitted (14-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                     Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
                                                                  oster, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E., Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E., Draper, H., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J., Hostin, D., Howland, T.J., Hume, J., Ibegwam, C., Jalali, M., Kovar, C., Liu, W., Mattei, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B., Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V. Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.
                                                                                                                                                       avy-Carroll,L., Dederich,D.A. Delanev r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
irza,N., Gill,K., Gulter, Harris,K., Hart,M.
imilton,K., Harris,C., Harris,K., Hart,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wheeler, D., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 161668)
Muzny,D., 'Scherer,S!, Adams,M.D., Holt,R.A., Evans
Goodyne,J.D., Tabor,P., Williamson,A., Homsi,F.H.,
                                                                                                                                                                                                                                                         enton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Busam, D.A., Center, A., Chen, G., Chen, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neopteara; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rogers, Y., An, H., Baldwin, D., Beeson, K.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ayele, M.A., Scott, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC104602

161668 bp DNA linear INV 06-A
Drosophila melanogaster X BAC RP98-16G6 (Roswell Park Cancer
Institute Drosophila BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dugan-Rocha, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC104602.3 GI:18030109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCCACATGAGTGGCAAGGCGTCTGGTGATACCG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Conservative
                                                                                                                                                                                                                        rter, M.,
                                                                                                                                                                                                                                                                                               sbrooks, S.L., Amaratunge, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 161668)
                                                                                                           n-Rocha,s.,
                                                                                                                                 A.L., Ding, Y.,
  ocha, S., Durbin, K.J... Earnhart, C., Edgar, D., Edwards, C.C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Harris, C., Harris, K., Hart, Havlak, P., Hawes, A.,
                                                                                                                                                                       Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Chavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
                                                                                                    ing,Y., Dinh,H.H., Douthwaite,K.J., Delgado,O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER44 repeat: matches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="FLAM_C repeat: matches 2. 30811. .30902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluJb repeat: matches 2.
30527. .30637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR_repeat: matches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.2%; Score 20.2;
75.8%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodergren, E.S., Hodgson, A.H., Chen, I
                                                                                                                                                                                                                                                                                                 Adio-Oduola, B., Ali-osman, F.R., Allen, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibbs, R. and Venter, J.
                                                                                                                                                                                                                                                                                  .C., Are, J.R., Banks, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hodgson, A.H., Chen, R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .128 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .234 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .108 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown, M., Buhay, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 106265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .106 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .131 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels , 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ecta; Pterygota;
Muscomorpha;
                                                                                                                                                     , Davis,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus
                                                                                                                                                                                                                                                                                  Barbaria, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INV 06-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brandon, R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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COMMENT

On Jan 1, 2002 this sequence version replaced gi:17976408 Submitted (06-APR-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA

Department

http://www.hgsc.bcm.tmc.edu/ or email

JOURNAL

Submission

Mel.G. Metzker, M. Miner, G., Mitchell, R. Metzker, M. Miner, G., Mitchell, R. Metzker, M. Miner, G., Mitchell, R. Metson, J., Newtson, J., Newtson, J., Newtson, J., Newtson, J., Newtson, J., Newtson, J., Neyton, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okuonu, G., Oragunye, N., Oviedor, R., Pace, A., Payton, B., Peery, J., Peters, I., Pickens, R., Primus, E., Pu, L. L., Rulz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tang, H., Tanssy, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tamall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walland, R., Wang, S., Walland, R., Washington, C., Walland, R., Wang, S., Walland, R., Walland, R., Washington, C., Walland, R., Walland, Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Liu, J., Liz, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martindale, Martindale, A., Martindale, Martindale, Martindale, A., Martindale, Martindale, Martindale, Martindale, Martindale, A., Martindale, M Wartinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao.T. Carria 1977. Submitted (01-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Dugan-Rocha, S., Denn, A.L., Ding, Y., Dinh, H.H., Worley, K.C.; Adams, C. Sisson, I., Somergren, E., Johnson, P., Tamerisa, A., Tamerisa, Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, H., Tansey, J., Taylor, C., Vera, V., Villalon, D., Vinson, P. Worley,K.C., Adams,C., Adio-Oduola,B., Alsbrooks,S.L., Amaratunge,H.C., Are,J. Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Orledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N. Watlington, S ter,M., Cavazos,S.R /-Carroll,L., Dederich,D.A., Detauey,...., e,S., Brieva,M., Brown,E. seged, H., Lozado, R. R., Wang, S., Ward-Moore, inez,E., Massey,E., Mawhiney,E., McLeod,M Submission ock, G. and Gibbs, R. Maheshwari, M., Mapua, , Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T. Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., H. Metzker, M. and Gibbs, R. Dathorne, S.R., ., Williams, G., Durbin, K.J., Miner, G., Miner, 2. Burrell, K.L., Byrd, N.C., Carron, T.F.,
R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Christopoulos, C., Cleveland, C.D., Cox, C.,
c B hard B hardla ur Bardla ur B Vasquez,L., Vera,V., Villatou,V., C., G-Moore,S., Warren,R., Washington,C., ims,G., Williamson,A., Wleczyk,R., Wooden,S., Blankenburg,K., Bonnin,D., Bouck,J., srown,E., Brown,M., Bryant,N.P., Buhay,C., ., Kureshi, A., Lichtarge, O., Lieu, C., Kelly David, R., Davila, M.L., Davis, C., Earnhart,C P., Martin, R., Martindale, A., Delaney, K.R., Delgado, O , Khan, U., Zhou, J., Zorrilla, S., Nelson, D. Vera, V., Villalon, D., Vinson, R., Lucier, A., Landry, N., Leal, B., Lewis, L.C. Johnson, R Ali-osman, F.R., , Mitchell, T., Mohabbat, K., , Edgar, D., Edwards, C. Banks, T Shen, H., Shooshtari, N., Gunaratne, P. King, L., Draper, H. Meador, M. Barbaria,J. Korvah, J., ., Liu,W. Hawes, A., Allen,C. Tamerisa, K. Luna, R., Hale, S.

REFERENCE AUTHORS

JOURNAL TITLE

SOURCE

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ORIGIN
                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                      Matches
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                  Local
   85717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUALSTAT-REPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   local mapping efforts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANNOTATION OF FEATURES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dentical matches are annotated as similar.
                                                                                                                                                  Similarity
                                  GCCACATGAGTGGCAAAGGCGTCTGGTGATACCG 33
GTCGGAGGAGTGGTACGGCGTCTGGGGATCCCG 85685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeats are identified using RepeatMasker (A. Smit and P. Green
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila
/db_xref="taxon:7227"
/chromosome="X"
                                                                                                                                                                                                                                                                  /function="polymorphic site"
36812 c 36365 g 43506 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                 note-"C/T"
                                                                                                                                                                                                                                                                                                                                                                                  function="polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="unresolved tandem repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="RP98-16G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unction-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unction="polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unction="polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ction="low quality region"
                                                                                                                                               61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .51271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .50534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .50507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    low quality region"
                                                                                                                                                  Score 20.2; DB 3; Length 161668; Pred. No. 2.2e+02;
                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster"
                                                                                                                   8;
                                                                                                                   Indels
                                                                                                                   0;
                                                                                                                Gaps
                                                                                                                   0,
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RESULT 15

664: contig of 664 bp in length

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AC087522/c
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Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown
Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Colli
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosenti, Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J. Travis, N., Triglilo, J., Vassiliev, H., Viel, R., Vo, Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
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O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 27, 2001 this sequence version replaced gi:14196392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, B., Wu, X., Wyman, D., Ye, w Zembek, L., Zimmer, A. and Zody, M.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ll repeats were identified using RepeatMasker:
nit, A.F.A. & Green, P. (1996–1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 177062 bases at least Q40 consensus quality: 177860 bases at least Q30 consensus quality: 178367 bases at least Q20
                                                                                                                                                                                                                                                                                                                       Insert size: 176000; agarose-fp
Insert size: 179152; sum-of-contigs
Quality coverage: 15.6 in 020 bases;
Quality coverage: 15.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L11867
Center clone name: 567_H_10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
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Search completed: July 10, 2003, 19:20:20 Job time: 294.951 secs
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Best Local S
Matches 25
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                                             65594 GCCACAGGAGGGCAGGTTGGTGATCCAG 65562
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765 1403: contig of 639 bp in length
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43601 c 43184 g 46106 t
                                                                                                           61.2%; Score 20.2; DB 2; Length 179752; 75.8%; Pred. No. 2.2e+02;
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_xref="taxon:9606"
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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                            Description
                                                                   Trichoderma reesei
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-	Drosophila melanog	Drosophila melanog	DNA encoding novel		Human immune respo	encoding	DNA encoding novel		DNA encoding novel	Human colon cancer	-deri		Human bone marrow	Human brain expres	Human foetal liver	Human immune/haema	DNA encoding novel	y chain	encoding r	pel	sy	RHDV capsid gene.	ctiv	Human nervous syst	Rice inositol 1,3,	Human cDNA encodin	Polynucleotide iso	Mouse genomic regi	DNA encoding novel	Arabidopsis thalia					

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## ALIGNMENTS

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Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno	(NECKY) NECKA CORE.	AND THE PROPERTY OF THE PROPER	03-DEC-1999; 99US-0168976.	07-JUN-1999; 99US-0137900.		05-JUN-2000; 2000WO-US15595.		14-DEC-2000.	WO200075333-A1.		Unidentified.	Streptomyces avidinii.	Synthetic.			Streptavidin; tumour cell; cancer; adenocarcinoma;		DNA encoding a fusion of a single chain antibody and streptavidin		02-APR-2001 (first entry)		AAC86584;	SUCCESSION SECTION 111 DE.	AAC86584 c+spdsrd. DNA. 771 BD	ULT 1

embryonic

XX

WPI; 2001-091213/10.

JM;

New vector constructs for expressing proteins which are useful for target

cancer,

e.g.

adenocarcinomas

targeting

genomic streptavidin

tumour cells associated with

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RESULT 2
AAA67547/c
ID AAA67547
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Best Local (
Matches 2
New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                              (GENE-)
(FLET-)
                                                                 WPI;
                                                                                       Bloksberg
                                                                                                                                                   13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                       08-OCT-1999;
                                                                                                                                                                                                                                                                                  Eucalyptus grandis; pinus radiat; plant cell wall; polysaccharide; transgenic plant; ds.
                                                                                                                                                                                                                 20-APR-2000.
                                                                                                                                                                                                                                       WO200022092-A2.
                                                                                                                                                                                                                                                               Pinus radiata.
                                                                                                                                                                                                                                                                                                                           Pinus radiata sucrose phosphate synthase DNA SEQ ID NO:548
                                                                                                                                                                                                                                                                                                                                                                                          AAA6754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  these are useful as purposes, e.g. for target site within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequence. Alternatively, the vector construct comprises a nucleic facid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells associated with cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linked to a promoter, and a cloning site for insertion of a succeic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a fusion of an anti-CEA single antibody and streptavidin: The fusion protein is expressed u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody and streptavidin. The fusivectors of the invention. The specifor expressing streptavidin fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                               2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adenocarcinomas or hematological malignancies. The vector construct setul for expressing of streptavidin fusion proteins. In particular, e are useful as tools for medical diagnostics and therapeutic
                                                                                                          GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                               2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                             339328/29
                                                                                                                                                                                                                                                                                                                                                                                                           Standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention. The specification describes vector constructs ressing streptavidin fusion proteins. The vector comprises a acid encoding streptavidin or its functional variant operatively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGATCAGCTGCAAGGCTTCTGGTTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACATGAGTGGCAAGGCGTCTGGTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 BP;
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                 98US-0170862
99US-0148426
                                                                                                                                                                                     99WO-NZ00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting the presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 180
                                                                                                          FORESTS
                                                                                                                                                                                                                                                                                                       radiata; Monterey pine;
                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 230 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19.8; DB Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches .
                                                                                                                                                                                                                                                                                             polysaccharide
                                                                                                          LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      absence of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                         biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or treating, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o;
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                                                                                                                                                                                                                                                                                       pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     second
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AAF15168/
ID AAF1
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                                                                                                                                                                                                8x2222222222222
                                                                                                                                 Matches
                                                                                                                                                               Query Match
                                                                                                                                                                                                                        AAA57073 to AAA67907, their (reverse) complements, sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences given in Expectation (E) value of 0.01 or less compared to the 835 sequences at least 50% identical to them, 200, 100, 40 or 20 mers of the to the 835 sequences that are degenerately equivalent or allelic activity of a polypeptide involved in a polypeat to modify the pathway in the plant. They are especially used to modify the polypaccharide content, composition or structure of the plant. AAB16360 are proteins encoded by some of the polynucleotide sequence given in the present invention.
                                                                                                                                                                                    Sequence 415 BP; 120 A; 85 C;
                                                                                                                                                                                                                                                                                                                                                           a sequence selected fr
AAA67073 to AAA67907,
                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                present invention describes isolated polynucleotides squence selected from one of 835 nucleotide sequences
                                                           156 CCATATGGGTGGCAAGGCTTTAGGAGATA 128
                                                                                                   N
                                                                                                                                  23;
                                                                                                                                              Similarity
                                                                                       CCACATGAGTGGCAAGGCGTCTGGTGATA 30
                                                                                                                                                                                                                                                                                                                                                                                                                    Page 212-213; 301pp;
                                                                                                                             Conservative
                                                                                                                                                                                                                       present
                                                                                                                                         58.8%;
79.3%;
                                                                                                                                                                                                                       invention.
                                                                                                                     Score 19.4; D
Pred. No. 69;
0; Mismatches
                                                                                                                            0;
                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                       <u>ი</u>
                                                                                                                                                                                    112 T;
                                                                                                                                                     B
                                                                                                                                                                                    0
                                                                                                                                                     21;
                                                                                                                                                                                    other,
                                                                                                                       6
                                                                                                                                                 Length
                                                                                                                   Indels
                                                                                                                                                   415;
                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                              comprising
                                                                                                                Gaps
                                                                                                                0,
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X PX X PX
                                                                            expressed sequence tag; Fusarium venenatum; Aspergillus niger. Aspergillus oryzae; Trichoderma reesel; identification; recombed culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering;
                                                         Trichoderma reesei
                                                                                                                           Multiple gene expression; expressed sequence tag; Fu
                                                                                                                                                                     Trichoderma
                                                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                             AAF15168
                                                                                                                                                                                                                                                  AAF15168 standard;
                                                                                                                                                                     reesei
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                cDNA; 634
                                                                                                                                                               SEQ ID NO:7691.
                                                                                                                                filamentous fungal
                                                                                                                                                                                                                                                BP.
                                                                                                                                cell;
                                                                                                  niger; recombination;
                                                                           SS
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WO200056762-A2

28-SEP-2000

22-MAR-2000; 2000WO-US07781

22-MAR-1999; 99US-0273623.

( OVON ) OVON NORDISK BIO BIOTECH INC.

WPI; 2000-594572/56 Berka RM, . Rey ¥, Shuster JR, Kauppinen 'n Clausen īĠ, Olsen

PB;

Claim ; 68 Page 3104; 3161pp; sequence English. tags

expressed

Monitoring differential expression of genes in filamentous uses fluorescence; labeled nucleic acids isolated from the

s fungal cells cells and a

expression of genes in a first filamentous rungal (re)
expression of the same genes in one or more second filamentous fungal
cells. The method uses fluorescence-labeled nucleic acids isolated from
the FF cells and a substrate of expressed sequence tags (EST). The ESTs
in a first filamentous fungal (FF) cell relative to expression of genes
in a first filamentous fungal (FF) cell relative to expression of the The present invention describes a method fo expression of genes in a first filamentous

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RESULT 4
AAFO7727
ID AAFO
XX AAFO
AC AAFO
AC AAFO
XX WALL
KW EXD
KW EXD
KW ASD
KW ASD
KW ASD
KW BO2
XX FUSI
XX
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Best Local S
Matches 24
The present inventor affirst filamentous tungal (rr) certaingal expression of genes in a first filamentous tungal (rr) certaingal expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The EST cells and a substrate of expressed sequence tags (EST) are the methods for monitoring differential expression of ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF0478 to AAF11247 represents ESTs from Apergillus Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF1337 represents ESTs from Trichoderma reeset, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200056762-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF07727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                 Claim 86; Page 478-479; 3161pp;
                                                                                                                                                                                                                                                                                                 Monitoring differential expression of genes uses fluorescence-labeled nucleic acids iso
                                                                                                                                                                                                                                                                                                                                                                                                                                             Berka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium venenatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF07727 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                          The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2000; 2000WO-US07781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tag; Fusarium venenatum; Aspergillus Aspergillus Aspergillus oryzae; Trichoderma reesei; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           culture condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                    2000-594572/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                             RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NOVO NORDISK BIOTECH
) NOVO NORDISK AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCACATGAGTGGCAAGGCGTCTGGTGATACC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGCAATAGCAGCAAGGCGTCTGGTGAGAGAGC
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                                                                                                                                                                                                                                                                    of expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway engineering;
                                                                                                                              invention describes a method for monitoring differential of genes in a first filamentous fungal (FF) cell relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           environmental stress;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Shuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.2%; Score 19.2; 75.0%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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usarium venenatum; Aspergil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al stress; spore more catabolic pathway
                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                       tags
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kauppinen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                              filamentous
ed from the o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Clausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                        IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    634;
                                                                                                                                                                                                                                                                                        s fungal cells
cells and a
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                                                The ESTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PB;
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genes

polypeptide (II) sequences: (I) is useful as hybridisation probes, polymerase chain reaction (PCN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags

Claim 1; SEQ ID No 1007; 103pp; English.

The invention relates to isolated polynucleotide (I) and

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RESULT 5
AAS65203/c
ID AAS65203 standard; c
XX AAS65203;
XC AAS65203;
XX DE DNA encoding novel h
XX Human; chromosome ma
KW Human; chromosome ma
KW Homo sapiens.
XX PN WO200175067-A2.
XX HOMO Sapiens.
XX HOMO Sapiens.
XX PF 30-MAR-2000; 2000US-PF 33-AUG-2000; 2000US-YR 31-MAR-2000; 2000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, diagnostics, forensics, gene mapping, identification or responsible for genetic disorders or other traits and biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 906 BP; 203 A; 271 C; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 GTCTCANAAGCCGCAAGGAGACTGGTGCTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCCACATGAGTGGCAAGGCGTCTGGTGATACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel human diagnostic protein #1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                               to assess
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                                                                                                                                                                                                                                                                                                                                   mutations
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RESULT 6
AAZ22700
ID AAZ2
XX AAZ2
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XX 15-F
XX ATP-
KW Micr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
    This sequence represents
                                        Claim 4;
                                                                             An ABC transporter gene -
                                                                     secrete
                                                                                                                                 WPI; 1999-626936/54
                                                                                                                                                                                                                          27-MAR-1998;
                                                                                                                    P-PSDB;
                                                                                                                                                             (TANA ) TANABE SEIYAKU CO.
                                                                                                                                                                                             27-MAR-1998;
                                                                                                                                                                                                                                                         12-OCT-1999
                                                                                                                                                                                                                                                                                     JP11276172-A
                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and disconsite coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ22700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ22700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical insigning of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics forements are manning interesting the polypeptide and polynucleotide sequences have applications in the diagnostics forements are manning identification of the polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                     proteins
                                                                                                               AAY55919, AAY55920,
                                      Page 12-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 5660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACATGAGTGGCAAGGCGTCTGGTGATACCG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1284 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cassette; transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fluorescens ABC | transporter cassette operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                          98JP-0080597
                                                                                                                                                                                                                         98JP-0080597
                                                                                                                                                                                                                                                                                                                                            /product= '3863..5197
                                                                                                                                                                                                                                                                                                                                                                                        2526..3860
                                                                                                                                                                                                                                                                                                                /product=
                                                                                                                                                                                                                                                                                                                                                                                                      /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 A; 308
                                  28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.2%;
75.0%;
        an
                                                                               used to increase
                                                                                                                                                                                                                                                                                                                                                         "component B"
                                                                                                                                                                                                                                                                                                               "component C"
                                                                                                                                                                                                                                                                                                                                                                                                      "component A"
   ATP-binding
                                                                                                               AAY55921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19.2;
Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 G; 311 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        operon; LipBCD; Serratia marcescens;
cassette (ABC) transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                            the ability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                          of a microbe to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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YA X PRXX
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ABN18387/c
ID ABN18387 standard; cDNA; 379
XX
AC ABN18387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                  syndrome associated with ORFX-associated disorder. ORFX pol
sequences can be used in gene therapy. ORFX sequences can t
treatment of cancer, hyperproliferative disorders, cirrhosi
psoriasis, benign tumours, keloid, degenerative disorders,
                                                                                                                                         The present invention describes substantially purified human (referred to as open reading frame, ORFX, where X is 1-11491 in the specification). ABN15762 to ABN27252 encode the human
                                                                                                    disorder
                                                                                                                                                                                                                   Disclosure; SEQ ID 5251; 1037pp;
                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                        in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
                                                                                                                                                                                                                                                                                                                                P-PSDB; ABP02635
                                                                                                                                                                                                                                                                                                                                             WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000; 2000US-206132P
29-AUG-2000; 2000US-228716P
                                                                                                                      reating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative disorder; psoriasis; benight thousas; haperproliferative disorder; psoriasis; benight tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; disheres mellitus; curtous; live disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myasthenia gravis; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX polynucleotide sequence SEQ ID NO:5251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5660 BP; 1131 A; 1817 C; 1736 G; 976 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             operon from Pseudomonas fluorescens strain 33. The operon comprises 3 genes where the termination codon of the first gene overlaps with the initiation codon of the second gene. The sequences of the encoded proteins have 60, 44 and 46% homology respectively to the tijbBCD proteins from Serratia marcescens. The novel gene and protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 GCCTCAGCAATGGCAAGCAGTCTGGTTTTACC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCCACATGAGTGGCAAGGCGTCTGGTGATACC 32
                                                                                       or preventing a pathology associated with an ORFX-associated in humans, and in the manufacture of a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              increase the ability of a microbe for secreting a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry
         neurodegenerative disorders
                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes mellitus; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFX; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19.2; DB 20
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                      cirrhosis of liver,
                                                                      ORFX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                         be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5660;
                                                                                     for treating a
                                                                                                                                                                              proteins
                                                                                                                                                             (see Table 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 8
AAS83486/c
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Best Local S
Matches 22
quantitating a a food sur-
           polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                                                                                                                                           Claim 1; SEQ ID No 19290; 103pp; English
                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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food supplement; medical imaging; diagnostic; genetic (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis.
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                    The present invention describes an expressed sequence tag (EST), wher the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell. Molecules which induce developmental competence in a cell line are useful for inducing totipotence in one or more cells. Molecules which induce developmental incompetence in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing developmental course cells of the animal into a specific cell type. The present sequence represents abvine EST which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the internation. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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	199	19	19	19	2-AUG-19	2-AUG-19	-19	-19	-19 -19	-19	<u>, i, ,</u>	22-JUL-19	<u></u> .	!	1	ر ئر ئ	<u>.</u> , . ,	ĻĻ,	- r	- 101-16	<u> </u>	<u>ٺ</u> ٺ.	المارك		2 2 :	4-JUN-1	77	JUN	JUN-	JUN-	-JUN-	22	-NOC-	-JUN-	NDC- NDC- NDC-	-JUN:	
	199	19	19	19	2-AUG-19	2-AUG-19	-19	-19	-19 -19	-19	<u>, i, ,</u>		<u></u> .	!		ء بر ب	<u>.</u> , . ,	ĻĻ,	<u>', ', '</u> ,	3 H L	<u> </u>	<u></u>	المارك		4 4	4 Z Z	77	JUN	JUN-	JUN-	-JUN-	22	77	Z Z :	NDC- NDC- NDC-	-JUN:	
	1999; 1999:	1999;	1999;	1999;	2-AUG-1999;	2-AUG-1999;	-1999;	-1999; -1999;	-1999; -1999;	-1999;	1999;	1999;	1999;	1999;	1999;	1999;	-1999;	-1999; -1999;	-1999;	1999;	1999;	-1999; -1999;	-1999; -1999;	1999; 1999;	V-1999;	N-1999; N-1999;	N-1999;	JUN-1999;	JUN-1999;	JUN-1999;	-JUN-1999;	N-1999;	N-1999; N-1999;	N-1999	-JUN-1999 -JUN-1999 -JUN-1999	-JUN-1999	
Ç	1999; 990 1999: 990	1999; 990	1999; 990	1999; 990	2-AUG-1999; 990	2-AUG-1999; 990	-1999; 990	-1999; 991	-1999; 991 -1999; 991	-1999; 99 -1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	-1999; 90 -1999; 90	-1999; 99 -1999; 99	1999; . 99	1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	N-1999; 9	N-1999; 9	N-1999; 9	JUN-1999; 9	JUN-1999;	JUN-1999; 9	-JUN-1999;	N-1999;	N-1999; N-1999;	N-1999;	-JUN-1999; -JUN-1999; -JUN-1999;	-JUN-1999;	
Ç	1999; 990 1999: 990	1999; 990	1999; 990	1999; 990	2-AUG-1999; 990	2-AUG-1999; 990	-1999; 990	-1999; 991	-1999; 991 -1999; 991	-1999; 99 -1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	-1999; 90 -1999; 90	-1999; 99 -1999; 99	1999; . 99	1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	N-1999; 9	N-1999; 9	N-1999; 9	JUN-1999; 9	JUN-1999;	JUN-1999; 9	-JUN-1999;	N-1999;	N-1999; N-1999;	N-1999;	-JUN-1999; -JUN-1999; -JUN-1999;	-JUN-1999;	
Ç	1999; 990 1999: 990	1999; 990	1999; 990	1999; 990	2-AUG-1999; 990	2-AUG-1999; 990	-1999; 990	-1999; 991	-1999; 991 -1999; 991	-1999; 99 -1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	-1999; 90 -1999; 90	-1999; 99 -1999; 99	1999; . 99	1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	N-1999; 9	N-1999; 9	N-1999; 9	JUN-1999; 9	JUN-1999;	JUN-1999; 9	-JUN-1999;	N-1999;	N-1999; N-1999;	N-1999;	-JUN-1999; -JUN-1999; -JUN-1999;	-JUN-1999;	
Ç	1999; 990 1999: 990	1999; 990	1999; 990	1999; 990	2-AUG-1999; 990	2-AUG-1999; 990	-1999; 990	-1999; 991	-1999; 991 -1999; 991	-1999; 99 -1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	1999; 99	-1999; 90 -1999; 90	-1999; 99 -1999; 99	1999; . 99	1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	-1999; 9 -1999; 9	N-1999; 9	N-1999; 9	N-1999; 9	JUN-1999; 9	JUN-1999;	JUN-1999; 9	-JUN-1999;	N-1999;	N-1999; N-1999;	N-1999;	-JUN-1999; 99US-0 -JUN-1999; 99US-0 -JUN-1999; 99US-0	-JUN-1999;	

99US-0149722 99US-0149723 9908-0149175. 99US-0148684. 99US-0149368. 99us-0149426.

0149929

-0148565 -0148341

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S
                      Query Match
Best Local S
       Matches
                                                                                                       L4 -OCT
                                                                                                                                                                                                               AUG
       Similarity 72.7
24; Conservative
1 GCCACATGAGTGGCAAGGCGTCTGGTGATACCG 33
                                 990S-0161361
990S-0161920
                      99US-0162142
                                        99us-0161360
                                                99US-0161406
                                                   990S-0161404
990S-0161405
                                                           99US-0160989
                                                               99US-01609B
                                                                                 99US-01607
                                                                                                                                                                                 -0153070
          56.48;
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                                                                             16077
                                                                                     L607
                                                                                        1607
                                                                                                       15933]
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                                                                                                                                                                                                           151066
                                                                                                               .59329
      Score 18.6; DB 21;
Pred. No. 1.7e+02;
0; Mismatches 9;
             Length 973;
       Indels
       0
      Gaps
      0
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RESULT 11
AAS83436/c
PR
                             밁
        31-MAR-2000;
23-AUG-2000;
                                                                                                                                            DNA encoding novel human diagnostic protein #19240
                                     30-MAR-2001; 2001WO-US08631.
                                                         11-OCT-2001
                                                                           WO200175067-A2
                                                                                             Homo sapiens.
                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                               13-FEB-2002
                                                                                                                                                                                  AAS83436;
                                                                                                                                                                                                      AAS83436 standard;
                                                                                                                                                                                                                                                   2000US-0540217.
2000US-0649167.
                                                                                                                                                               (first entry)
                                                                                                                                                                                                     CDNA; 1122 BP.
                                                                                                                                                                                                                                                   236
                                                                                                                  SS
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity biodiversity

Drmanac RT, Liu C,

Tang YT;

2001-639362/73. DB; ABG19249.

(HYSE-) HYSEQ INC.

Claim 1; SEQ ID No 19240; 103pp; English

CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, are also used in diagnostics as expressed sequence tags (C to restore normal activity of (II) is useful in gene therapy techniques (C II). (II) is useful for generating antibodies against it, detecting or creating of sites expressing (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cast introub, but was obtained in electronic format directly from WIPO at fravelonic to the printed of the product of the printed cast of the invention. at ftp.wipo.int/pub/published\_pct\_sequences. The invention on relates to isolated polynucleotide (I) and (II) sequences. (I) is useful as hybridisation probes,

Sequence 1122 BP; 216 A; 400 C; 309 G; 196 T; 1 other;

δÃ Query Match Best Local S Matches 24 Similarity 56.4%; nilarity 72.7%; Conservative 0 Score 18.6; DB 23; Pred. No. 1.8e+02; 0; Mismatches 9; 33 Length 1122; Indels 0 Gaps

0

밁 GCCACATGAGTGGCAAGGCGTCTGGTGATACCG

1074 GCCACAGGAGTCGGCTGCGGTCTGTTTATACCG 1042

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RESULT 13
AAA96719/c
ID AAA0677
                                                                                                                                                                                                                                       CC compound upon a transmembrane which expresses a taste cell specific ion cc compound upon a transmembrane ion flux of a predetermined ion, cc compound upon a transmembrane ion flux of a predetermined ion, cc (M1) is useful for identifying a compound that modulates taste signalling in taste cells. CC in taste cells, for identifying a compound that modulates taste signalling cc specific ion channel subunit, and for modulating taste signalling in taste cells of a mammal, in particular a human Modulators identified by (M1) cc are used by the food and pharmaceutical industries to customize taste. CC different to the subject who ingests it. Bitter medicines can be made to customize teste to taste less bitter and sweet substance can be enhanced. The modulators are conjects for modulation of taste signalling cc subjects for modulation of taste in vivo. The present sequence is that of the mouse general to a taste in the present sequence is that of the mouse general reason modulators can be directly administered to mammalian contains the invivo. The present sequence is that of
                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
ABN85733/c
ID ABN85733
                                                                                                                                                                   Matches
       AAA96719
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to identifying (MI) a compound that modulates task signalling in taste cells, by contacting the compound with a eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying modulators of taste signaling in taste cells for use in food and pharmaceutical industries to customize and regulate taste, by determining effect of the compound on a taste cell-specific ion channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC,) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-2000;
21-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2001; 2001WO-US49808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO20025,4069-A1
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                                                                                                                                                                                    Loca L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          taste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP | 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN85733;
                                                                                                                                                                 21
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ltrpc5; taste
cell-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic region
   standard;
                                                                                   ACAGGAGTGGCAAGGTGTATGGGGA
                                                                                                                   ACATGAGTGGCAAGGCGTCTGGTGA 28
                                                                                                                                                                                                                               249487;BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002.
                                                                                                                                                                                                                                                          genomic region containing the ltrpc5 gene of the inve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 249487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 64-207; 306pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-259379P
2001US-0026188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      taste; cell|signalling; TC:ICS; food; pharmaceutical;
DNA;
                                                                                                                                                                                                                      64808 A; 61913 C; 61498 G; 61236 T;
                                                                                                                                                                          56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion channel subunit;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              containing the ltrpc5 gene SEQ
1131
                                                                                                                                                         Score 18.6; DB
Pred. No. 3.8e+C
0; Mismatches
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                                                                                                                                                                        8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a compound that modulates taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds.
                                                                                                                                                                            Length 249487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO
                                                                                                                                                                                                                    32 other;
                                                                                                                                                 0,
                                                                                                                                              Gaps
                                                                                                                                                0
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GCCACATGAGTGGCAAGGCGTCTGGTGA 28

Matches Query Match

Local.

Similarity

55.8%; 78.6%;

Score 18.4; Pred. No. 2 Mismatches

2e+02 DB 21; 6;

Length 1131;

0;

Gaps

0;

Conservative

0,

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CC isolated from lymph node stromal cells of fsn // mice. The CC polynucleotides and their polypeptides are useful for treating an CC inflammatory disorder, disorder of immune system and cancers, a from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a CC growth of blood vessels. The polypeptides are useful for treating an CC growth of blood vessels. The polypeptides are useful for treating a CC growth of blood vessels. The polypeptides are useful for treating a CC from arthritis, inflammatory bowel disease and cardiac failure and a CC fibroblast growth factor-mediated disorder, such as those selected CC fibroblast growth factor-mediated disorder. It is also useful in assays CC corresponding ligands or receptors, to quantify levels of protein or CC cognate corresponding ligand or receptors, as antinflammatory agents, cand in compositions for the treatment of skin, connective tissue and CC tissue, as a chromosome marker or tags in the identification of a xxx genetic disorder.
              Sequence 1131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 35; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide expressed in mammalian fsn -/- lymph node stromal cells, useful for modulating growth of blood cells, for treating inflammatory and tumour necrosis factor-mediated disorders, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-664924/64.
P-PSDB; AAB19109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strachan L,
Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999;
26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200058463-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immure system disorder; cancer; viral disorder; HIV infection; blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor mediated disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lymph node stromal cell; fsn -/- mice; immune system disorder; cancer; viral c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide isolated from lymph node stromal cells of fsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0383586.
              208
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1..360
            Α,
343 C; 342 G; 238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abernethy N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory
disorder; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumble
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AAF93747 standard; cDNA; 3425

Human; secretory protein; membrane protein; vaccine; gene therapy rheumatoid arthritis; diabetes; ss.

Human cDNA encoding a membrane or secretory protein clone PSEC0007

(first entry)

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Вb
                                                                                                                Query Match
Best Local Similarity
                                                                                              Matches
                                                                                                                                                                                        Sequence 3425 BP;
                                                                                                                                                                                                                                                    protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies and antagonists may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB8317 - AAB88419. Included in the invention are primers AAF94295 and AAF62232 - AAF62235 which are used to isolate to CDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 7; 609pp + CD ROM; English.
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11-JAN-2000;
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  1891
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GCCACCTGTGTGGCAAGACGTGCAGTGA 1918
                                            GCCACATGAGTGGCAAGGCGTCTGGTGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 99JP-0194179.
; 2000JP-0118775.
; 2000JP-0183766.
                                                                                                                                                                                                                                       diabetes.
                                                                                                                                                                                     800 A; 840 C; 917 G;
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                                                                                                             55.8%;
78.6%;
                                                                                                             Score 18.4;
Pred. No. 2.
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                                                                                            Mismatches
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                                                                                                                                                                                     868 T; 0 other;
                                                                                                                  .5e+02
                                                                                                                                           DB
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                                                                                                                                      22;
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                                                                                                                                      3425;
                                                                                       0
                                                                                         Gaps
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RESULT 15 AAZ48806

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Query Match Best Local Matches

20;

Conservative

0;

Similarity

55.2%; 87.0%;

Score 18.2; DB 21 Pred. No. 2.4e+02; Mismatches

DB 21;

Length Indels

518; 0;

Gaps

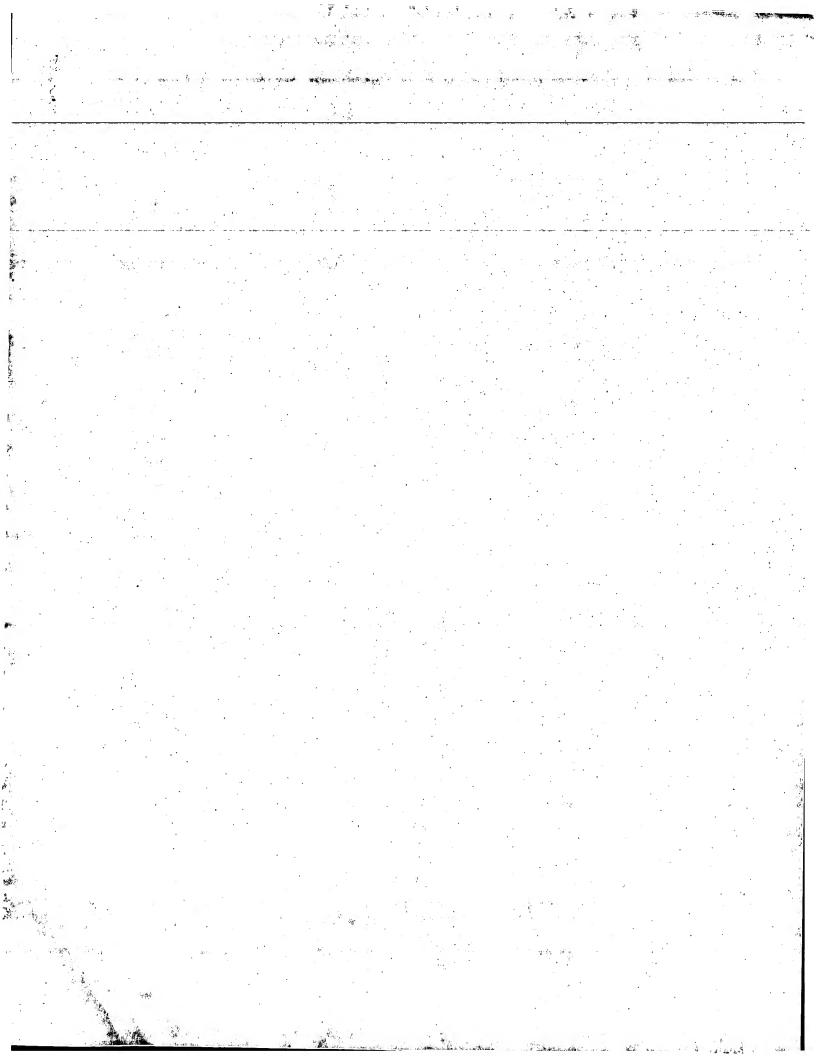
0;

Search completed: July 10, 2003, 19:52:39 Job time: 72.6337 secs

198 CATTAGTGGCAAAGCCTCTGGTG

5 CATGAGTGGCAAGGCGTCTGGTG 27

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XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes an inositol 1,3,4-triphosphate 5/6-kinase (ITK) CC protein of the invention. ITK is a phytic acid (Myo-inositol 1,2,4,5,6-hexaphosphate) biosynthetic enzyme. The ITK enzymes of the CC 1,2,3,4,5,6-hexaphosphate) biosynthetic enzyme. The ITK enzymes of the CC invention may be prepared recombinantly and used to raise antibodies, CC which are used for detecting the enzymes in situ in cells or in vitro CC in cell extracts. The polynucleotides of the invention may be used to CC create transgenic plants in which the ITK levels are present at higher CC viewer levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of CC 1,3,4-triphosphate 5/6 kinase found in those cells. In addition, it may CC be desirable to eliminate expression of ITK genes for certain applications. The polynucleotides of TK genes for certain CC inked to those genes, and to isolate homologous sequences from other CC species, as well as for physical mapping, as markers for traits candinated to improved feed efficiency. The proteins of the present contribution lead to a better understanding of the phytic acid biosynthesis of anathur, allowing it to be exploited for commercial uses. A in a final continual contribution is a supplication of the present contribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inositol 1,3,4-triphosphate 5/6-kinase; phytic acid; genetic myo-inositol 1,2,3,4,5,6-hexaphosphate; biosynthetic enzyme; animal feed; ss.
Sequence 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 45; 63pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel phytic acid biosynthetic enzymes used enzyme in transgenic plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-1998;
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                                                           pathway, allowing it to be exploited for commercial uses, e.g. in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ48806 standard; cDNA; 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlson IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .(first_entry)
BP; 120 A; 114 C; 117 G; 159 T; 8 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US08790
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phytate;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
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                                                                                        gccacatgagtggcaaggcgtctggtgataccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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19227
40138
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US-09-221-017B-615

US-09-671-376C-4

US-09-090-793-13

US-09-090-793-13

US-09-103-18408-2

US-09-103-8408-2

US-09-103-8408-1
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396, App
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Query Match
Best Local Similarity
Matches 22; Conserv
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                                                           MOLECULE NO HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD AND PROBES FOR INVENTION: OF MICROBIAL GENES SPE
                                                                                                             STRANDEDNESS:
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o. 6365401
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1900 Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08651155B
                                                                                                                                                                                                                                                                                                                                                                                                       USA
  Conservative
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Conner Mr., Christopher
Hiethoff Mr., Douglas M.
                                                                                                    linear
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17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	
51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	51.5	
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US-08-734-344-1	US-08-653-650A-4	US-09-096-982-4	US-09-206-942-29	US-09-206-942-31	US-08-653-650A-7	US-09-096-982-7	US-08-907-740-5	US-09-020-818-5	US-08-596-024-5	US-08-329-055-5	US-08-837-058-10	US-09-041-889-10	US-08-480-753-5	US-08-329-055-2	US-09-385-982-397	US-08-468-671-15	US-08-259-372A-15	
Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	29,	Sequence 31, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 5, Appli	Seguence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 5, Appli	Sequence 2, Appli	Sequence 397, App	Sequence 15, Appl	Sequence 15, Appl	

## ALIGNMENTS

FOR THE IDENT:

IDENTIFICATION
ICALLY INDUCED DURING

HOST

P.C.

```
NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 36,238
REFERENCE/DOCKET NUMBER: 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
TELEFAX: 303/449-5426
                                                                                                                                                                                                                                         TELEX: ABA1475
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,155B
FILING DATE: 17-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Petersen Mr., Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 nucleic acid
                                                                                                                                                                single
                                                                                                                             (genomic)
                   55.8%;
78.6%;
Score 18.4; D
Pred. No. 19;
0; Mismatches
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                                    DB
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                                  Length 320;
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6

Indels

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; ORGANISM: Mouse
JS-09-383-586-7
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Best Local S
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                                                   REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                               TELEPHONE:
                                                                                                        CLASSIFICATION:
                                                                                                                    FILING DATE: 06-JU
                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                             TNG SIGNATURE: PETENTIAN Release APPLICATION DATA:
APPLICATION DATA:
US/08/471,025
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                                                                                                                                                                                                       READABLE FORM:
                                                                       frommer, William S.
                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              586-7
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                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGATGAGTGGGACGGAGTCTGCGGA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                530 Fifth Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strachan, Lorn
Sleeman, Matth
                                                                                                                                                                                                                       United States of America
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                                                                                                                                                                                                                                                                                                                                                                 Fischer,
                                                                                                                                                                                                                                                                                                                                                                           Paoletti, Enzo
                                                                                                                                                                                                                                                                                                 .09105, Francois-Xavier
1MTION: RECOMBINANT POXVIRUS - CALICIVIRUS
1MTION: [RABBIT HEMORRHAGIC DISEASE VIRUS (RDHV)] COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                      06-JUN-1995
N: 424
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                                                                                                                                           Release #1.0, Version #1.30
                                                                                                                                                                                                                                                          Morris & Safford, P.C.
Avenue, 25th Floor
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78.6%;
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Pred. No. 24;
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RESULT 5
US-09-385-982-396
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Query Match
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US-08-276-967-1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                          OLECULE TYPE:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           Local
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                              STRANDEDNESS:
                                                                                                    LENGTH:
                                                                                                                                                                             NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
                                                                                                                                                             ECOMMUNICATION INFORMATION: FELEPHONE: 713-787-1400
                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Submi
                                                                                                                                                       ELEFAX:
                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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MATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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87.0%;
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  Score 18.2;
Pred. No. 4
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Pred. No. 32;
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         Length 7785;
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509 GTGGCCAGGCGTCTGGTGCAACC 531

10 GTGGCAAGGCGTCTGGTGATACC 32

Conservative

Mismatches

Indels

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Gaps

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; OTHER INFORMATION: n - A,T,C or
US-09-385-982-396
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LENGTH: 617
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Patent No. 6262334
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-872-719-1
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                                                                    NFORMATION FOR SEQ ID NO:
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARLIER APPLICATION NUMBER: ARLIER FILING DATE: 1999-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: ENDEGE, WILSON O., ET AL.
ITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
ITLE OF INVENTION: PRODUCTS: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URRENT FILING DATE: 1999-08-30 ARLIER APPLICATION NUMBER: 09/ARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ent No.
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                     TELEPHONE:
                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: HOUSTON
   STRANDEDNESS
                                                                                                                                   REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-01-27
APPLICATION NUMBER: 60/098,639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/385,982
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                                                                                                                                                                                                                                                                                                                                                                77057-2198
              nucleic acid
                                                                                                                                                                    Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08872719
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                                                                                    (713)
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                                                                                                   (512) 418-3000
                                                                                                                                                                                                                          CONCURRENTLY HEREWITH
single
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                                                                                                                                                    37,642
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                                                                                                                                     INDY: 012PZ1
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Pred. No. 40;
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Matches
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            CORRESPONDENCE ADDRESS:
                              NUMBER OF SEQUENCES:
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ADDRESSEE:
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RESULT 8-
US-09-336-890-1
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                                                          Sequence 1, Application US/09336890 Patent No. 6190661
GENERAL INFORMATION:
APPLICANT: Kelley,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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APPLICANT: William
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                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
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                                                                                                                                                    821 GCCACAAGAGCGCCAAGGCTTCGGGGAAT 849
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                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Concurrently Herewith
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           MARK R. METHODS AND COMPOSITIONS FOR THE USE
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75.9%;
 APURINIC/APYRIMIDINIC
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Pred. No. 4
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ARNOLD, WHITE & DURKEE O. BOX 4433

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Best Local S
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: IND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: IN
                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                 FILING DATE:
                                                                                 APPLICATION NUMBER:
                                                                                                                  CLASSIFICATION:
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                    XI
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCES:
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75.9%;
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                                                                                   08/957,302
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                 37,642
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Pred. No. 4
   INDY: 005
                                                                                                                                                                                                                                                                                                                                                   DURKEE
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                                                                                                                                                                                    Version #1.30
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RESULT 11 US-08-957-302A-3

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Best Local Similarity 75.9%;
                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6406917
                                                                                                                                                                                                               TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (713) 789-2679
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. B
CITY: HOUSTON
STATE: TEXAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                        NAME: Highlander, Steven REGISTRATION NUMBER: 37,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                        Local Similarity
                                                                                                                                                   LENGTH: 1279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 77057-2198
                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/668,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                      ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821 GCCACAAGAGCGCCAAGGCTTCGGGGAAT 849
821 GCCACAAGAGCGCCAAGGCTTCGGGGAAT 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCCACATGAGTGGCAAGGCGTCTGGTGAT 29
                                                             22;
                            1 GCCACATGAGTGGCAAGGCGTCTGGTGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09668499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEXAS .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: ARNOLD, WHITE & DURKEE P.O. BOX 4433
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                                                             Conservative
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                                                                                                                                                                                                                                             (512) 418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARK R. METHODS AND COMPOSITIONS FOR THE USE OF APURINIC/APYRIMIDIN
                                                                           53.9%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                   08/872,719
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Pred. No. 45;
                                                                           Score 17.8;
Pred. No. 4
                                                             Mismatches
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BB
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                                                               Indels
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Best Local 9
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                                                                                                                                                                                                                                                                                                           TELEFAX: (713) 789-26
NFORMATION FOR SEQ ID NO:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      NERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                CURRENT APPLICATION DATA
                                                                                                                                                                                                       ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                       PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                         ITLE OF INVENTION:
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                                                                                                       COUNTRY: US
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1395 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                         CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: Concur
APPLICATION NUMBER:
                                                                                                                                                                           STREET:
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                                                                                                                                                                                          DDRESSEE: ARNOLD,
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                                                                                                                                                                                                                                                                                                                                                                                                                    1137 GCCACAAGAGCGCCAAGGCTTCGGGGAAT 1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCACATGAGTGGCAAGGCGTCTGGTGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 75.9
22; Conservative
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                                                                                                                                                                                                                                                                     Williams, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ghlander, Steven L.
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                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                       Kelley, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                     DNA Sequences Encoding Fusions of DNA Repair Proteins and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.9%; Score 17.8; 75.9%; Pred. No. 46;
                                                                                                                                                                                        WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHITE & DURKEE
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US/09/542,403
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                             Version #1.30
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US-08-957-302A-1
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Best Local Similarity /3.,
Best Local Similarity /3.,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                       TELEFAX: (713) 789-26 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORRESPONDENCE ADDRESS
                         STRANDEDNESS:
                                                                                                                                                     NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/957,302A
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                           77210-4433
                                        nucleic acid
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                                                                                                                        (512) 418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WHITE & DURKEE
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Pred. No. 4
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Query Match
Best Local Similarity

53.9%;

Score 17.8; Pred. No. 4

BB

Length 1575;

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Gaps

0;

Mismatches

Matches

Conservative

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Query Match
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MEDIUM TYPE: Floppy disi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                             TITLE OF INVENTION: P. NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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22; Conserv
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94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TION NUMBER: 37
E/DOCKET NUMBER:
                          CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATION:
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WENTION: DNA Sequences Encoding Fusions of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ION NUMBER:
                                                    755 PAGE MILL ROAD
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                                                                                                                                                                  Application US/09221017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (713) 789-2679
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              USA
                                                                                                                          Ross, Bruce C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steven
                                                                                                                                                                                                                                                                                                          53.9%;
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                                                                                                              GINGIVALIS NUCLEOTIDES AND USES THEREOF
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Pred. No. 47;
0; Mismatches
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Matches
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-DEC-1997 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MONTOY, GLACY:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1...949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                        ORGANISM:
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829 GCAATATGATTGCCAAGGAGTTTGCGGATAAC 860
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                              1 GCCACATGAGTGGCAAGGCGTCTGGTGATACC
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Pred. No. 53;
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Search completed: July 10, 2003, 20:27:34 Job time: 34.7573 secs

Gaps

US-09-878-574-3877

Sequence 1205, Ap Sequence 1205, Ap Sequence 1359, Ap Sequence 2448, Ap Sequence 2448, Ap Sequence 1448, Ap Sequence 1448, Ap Sequence 12260, App Sequence 12260, App Sequence 69, App Sequence 69, App Sequence 187, App Sequence 1603, Ap Sequence 1603, Ap Sequence 20104, App Sequence 20104, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 4422, App

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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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US-10-087-631B-12
US-10-087-631B-15
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US-10-995-598-85
US-09-995-598-87
US-09-995-598-89
US-09-918-995-25170
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US-10-144-649A-746
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Sequence 5, Appli
Sequence 12, Appl
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Sequence 81, Appl
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Sequence 88, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 25170, A
Sequence 716, App
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Sequence 15103, A
Sequence 1, Appli
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                                                             Sequence 12, Application US/10087631B
Publication No. US20030054372A1
GENERAL INFORMATION:
APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10087631B Publication No. US/20030054372A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 33
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                                                                                                                                                                                                                  Matches
                          TITLE OF INVENTION: A METHOD FOR TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A METHOD FOR THE DETERN TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999 CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01 NUMBER OF SEQ ID NOS: 17
  CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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A NUCLEIC ACID USING

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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: amplification control having a bind: OTHER INFORMATION: internal region being parallel-complus-10-087-631B-14
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US-10-087-631B
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LENGTH: 24
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                                                                                                                                                        SOFTWARE: PatentIn version 3.1 EQ ID NO 14
                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
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                                                                            FEATURE:
                                                                                              ORGANISM: Artificial Sequence
                                                                                                                    TYPE: DNA
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                Description of Artificial Sequence: ICSJ620 HCV (HCV specific amplification control having a binding site for ST280 and ST778 internal region being parallel-complement to HCV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
97.1%;
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Pred. No. 1.3;
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   Query Match
Best Local Similarity
                                                                                                                                                                        SEQ ID NO 85
LENGTH: 744
                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-03-
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence \cdot 11, Application US/10087631B Publication No. US20030054372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-995-598-85/c
                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/253741 PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-11-29
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ENTEROVIRAL POLYNUCLEOTIDES, TITLE OF INVENTION: CONTAINING THE POLYNUCLEOTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/087,631B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A METHOD FOR THE DETERMINATION TITLE OF INVENTION: CONTROL
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CRAINIC,
                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: QS (pc) OTHER INFORMATION: complement to according region of HCV type 1
                                                                                      NAME/KEY: CDS
LOCATION: (1)
                                                                                                                       FEATURE:
                                                                                                                                     ORGANISM: Echovirus
                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 GCCACATGAGTGGCCAAGGCGTCTGGTGATACCG
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                          PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                 CARO,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09995598
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                                                                                                                                                                                                                                                                                                                                                                              VALERIE
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97.1%;
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97.1%;
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Score 20;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 9; Length 943; Pred. No. 1.4;
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                 Length 744;
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Matches .

5 CATGAGTGGCAAGGCGTCTGGTGATACC

32

0;

Mismatches

5

Indels

0

Gaps

436 CATGAGTGGCGAGGTGTCTGTTGACAAC

409

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FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(744)

OTHER INFORMATION:

US-09-995-598-87
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Sequence 87, App
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                                                                                                               US-09-995-598-89
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APPLICANT: CRAINIC, RADU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                 Query Match
Best Local
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                                                  Matches
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                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(744)
OTHER INFORMATION:
                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/253741
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 96
SOFTWARE: DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/995,598
CURRENT FILING DATE: 2001-11-29
                                                                                                                                                                                                                                                        SOFTWARE:
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PRIOR FILING DATE: 2000-11-29
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                                                                                                                                                                                       ORGANISM: Echovirus
                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                               PPLICANT: CARO, VALERIE
PPLICANT: GUILLOT, SOPHIE
ITLE OF INVENTION: ENTEROVIRAL POLYNUCLEOTIDES, MEITLE OF INVENTION: CONTAINING THE POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Echovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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PPLICANT: GUILLOT, SOPHIE

TILE OF INVENTION: ENTEROYURAL POLYNUCLEOTIDES, MEI

ITLE OF INVENTION: CONTAINING THE POLYNUCLEOTIDES

ILLE REFERENCE: 215059US-660-660-0
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ent No. US20020142293A1
                                                                                                                                                                                                                           ENGTH: 744
                                                                                                                                                                                                                                                                                                                                                    LE REFERENCE: 215059US-660-660-0
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                                                                                                                                                                                                                                           1D NO 89
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 5 CATGAGTGGCAAGGCGTCTGGTGATACC 32
                                                 23; Conserv
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                                                              60.6%;
                                               Score 20; DB:
Pred. No. 11;
0; Mismatches
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Pred. No. 11;
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                                                                           Length 744;
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                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
US-10-150-762-38
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Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                    ILE REFERENCE: 690022.547C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Goshorn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION:
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                                                              Similarity
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CCACATGAGTGGCAAGGCGTCTGGTGATACC 32
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                                                                                                                                                                                                                                                                                                                                                                                                                Schultz,
                                                                                                                                                                                                                                                                                                                                                                                                                               Graves,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schultz, Joanne Elaine
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                                                                                                                                                                                                                                                                                                                                                                                              Lin, Yukang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reno, Jonh M.
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yukang
                                                                                                                                                                                                                                                                                                                                                                                                                              Scott S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephen C
                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephen C.
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                                                          60.0%;
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                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 38 LENGTH: 771
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS ITLE OF INVENTION: METHODS OF USE THEREOF THE REFERENCE: 690022.547C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 CATGAGTGGCGAGGTGTCTGTTGACAAC 409
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C: Dearstyne, Erica A.
INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND INVENTION: METHODS OF USE THEREOF
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No. US20030095977A1
                                                                                                  PRIA3 single chain antibody-genomic Streptavidin fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIA3 single chain antibody-genomic Streptavidin fusion construct
Score 19.8; D
Pred. No. 14;
0; Mismatches
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Pred. No. 14
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                                       Length 771;
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US-10-144-649A
                                                              RESULT 13
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                                                                                                                                                                                                 TYPE: DNA | OTHER INFORMATION: Clone ID: 57-LIB188-003-Q1-E1-G10 US-09-960-352 13265
                             Sequence 746
GENERAL INFO
                  Publication
                                                                                                                                                                  Matches
                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                               SEQ ID NO 13
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CURRENT FILING DATE: 2001-0
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                                                                                                                                                                                                                                                                                                            UMBER OF
                                                                                                                                                                                                                                                                                                                                     PLICANT: Mathialagan, Nagappan
(TLE OF INVENTION: NUCLEIC ACID AND OTHER MOLE
(TLE OF INVENTION: NUCLEI AND FAT DEPOSITION
(ILE REFERENCE: 16511.006/37-21(1028))
(ILE REFERENCE: 16511.006/37-21(1028))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 499
                                                                                                                                                                                                                                                                                   ENGTH: 405
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LOCATION: (1)...(499)
OTHER INFORMATION: n = A,T,C
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blication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Hyseq, Inc.
ITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED.
ITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
ILE REFERENCE: 20411-756
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                             Similarity
                                                                                                                         GCCACATGAGTGGCAAGGCGTCTGGTGATACC 32
                                                                                            GCCATATGGGTGGCATGGTGCCTGGGGCTGCC 144
 RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US20020137139A1
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         Application US/10144649A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATAAGTAACAAGGCTTCTGGTGAGATC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATGAGTGGCAAGGCGTCTGGTGATACC 32
                                                                                                                                                                                                                                                                                                                                                                                                            Byatt, John C
                                                                                                                                                                                                                                                                                                                                                                                                                             Tao, Nengbing
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                                                                                                                                                             Conservative
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                                                                                                                                                                      58.2%; Score 19.2; 75.0%; Pred. No. 2
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79.3%;
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Pred. No. 2
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                                                                                                                                                                                Length 405;
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                                               RESULT 15
US-10-156-761-15103/c
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               Sequence 15103, Application US/10156761 Publication No. US20030119018A1
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; NAME/KEY: CDS
; LOCATION: (1)..(1197)
US-10-156-761-409
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                                                                                  Query Match:
Best Local S
                                                                    Matches
                                                                                                                                                                                                                           SEQ ID NO 409
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                     UMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 746
LENGTH: 161280
                                                                                                                                                                      EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0-156-761-409/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
                                                                                                                                                                             RGANISM: Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRILICANT: Algate, Paul A.
PRILICANT: Algate, Patricia D.
ITLE OF INVENTION: COMPOSITIONS
ITLE OF INVENTION: THE THERAPY
ITE DEPERATORS
                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ence 409, A
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1019 GCCAGATGCGGGGGGGGGGGTGAGTGATGTCG 987
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nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                            1 GCCACATGAGTGGCAAGGCGTCTGGTGATACCG
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/156,761 FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CCACATGAGTGGCAAGGCGTCTGGTGA 28
                                                                             Similarity
                                                                                                                                                                                                                                                                                        ICATION NUMBER: JP 2001-204089
                                                                                                                                                                                                                                                                                                                                                                                                               ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                               Conservative
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                                                                         Score 18.6;
Pred. No. 51;
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Pred. No. 48;
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                                                                                    DВ 9;
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SATOSHI

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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIXAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compugen Ltd
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AQ989608 Rfc00171
AW804244 PM3-UM008
AZ922863 SLCot5F03
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## ALIGNMENTS

REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM RESULT 1 AV736417/c LOCUS DEFINITION ACCESSION VERSION FEATURES TITLE source AV736417
AV736417 CB Homo sapiens cDNA clone CBNBDB05 5', mRNA sequence.
AV736417 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Contact: Zhu Chen Shanghai Institute of Hematology, Rui-Jin Hospital 197 Rui-Jin II Road, Shanghai 200025, P. R. China Tel: 86-21-64740490 1 (bases 1 to 615)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q.,
Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong. Fax: 86-21-64743206 Email: mbshi@ms.stn.sh.cn Unpublished (2000) AV736417.1 This clone is available at Shanghai Hematology Institute Location/Qualifiers ∕organism="Homo sapiens" GI:10853998 Zhou, J., Shen, Y., Han, Z., EST 17-OCT-2000

Funayama, T

Euteleostomi; Murinae; Aizawa, K.,

Oda, H.,

Kawai, J. Owa, C.

Hara SnW

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DEFINITION - AV003500 Mus musculus
                                                                                                                                                                                                       Similarity
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                                                                                                                 CAACATGAGTGGCGATGCGACTGGTGATGCAG 259
                                                                                                                                     CCACATGAGTGGCAAGGCGTCTGGTGATACCG
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Mycosphaerella graminicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   son, J.P.R., Bailey A.M. and Hargreaves, J.A. group of expressed cDNA sequences from the wheat fungal leaf lotch pathogen, Mycosphaerella graminicola (Septoria tritici) angal Genet. Biol. [29 (2), 118-133 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -Long Ashton Research Station
Ashton, Bristol, BS41 9AF, UK
+44(0)1275 392181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pSPORTI; Library constructed from cultures utilizing ammonium ions as a source of nitrogen" 155 c | 160 g | 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hargreaves JA
                                                                                                                                                                                                                                                                                                          /clone_lib="MgA Library"
                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:54734"
/clone="MgA0121"
                                                                                                                                                                                                                                                                                                                                                           /organism="Mycosphaerella
/strain="Strit"
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Tector: pBluescript; Site_1: EcoRI; cloned randomly with the EcoRI digestion" 194 c 105 g 146 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                               . 587
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                                                                                                                                                                             67.9%; | Score 22.4; L
81.2%; Pred. No. 92;
tive 0; Mismatches
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                  C57BL/6J kidney Mus musculus
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Pred. No. 78;
                                      211 bp
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                              EST 24-AUG-1999
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Photorhabdus luminescens
                                                                               Rfc00171
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                              AQ989608.1 GI:9648202
                                                    AQ989608
                                                         Photorhabdus luminescens
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                   GCCACATGAGTGGGANGGATTCTGCTGATTC 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostabilization and thermoactivation of thermolabile enzymes trehalose and its application for the synthesis of full length cr(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
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Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y.,
A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M.
Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,
Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Mouse ESTS
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Muramatsu,M., Okazaki,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        visit our web site (http://genome
                                                                          Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                T 3/]; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mus musculus C57BL/6J kidney"
/tissue_type="kidney"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="0610030E08"
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Rodentia; Sciurognathi;
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                                                           genomic clone
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Ed
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                                                                        strain W14
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                                                  PLG00171, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for DNA sequencing using RNA S.A. 95(7):3455-3460 (1998))
                                                                                                                                                                                                                                                           Length 211;
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Itoh,M., Izawa,M.,
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RESULT 3 AV003500/c

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ORIGIN

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Query Match Best Local

Matches

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
                                                                                                                                                   Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.E., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia;G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                        EST.
                                                                                                                                                                                                                                                                                                                                                        AW804244.1
                                                                                                                                                                                                                                                                                                                                                                                   AW804244 118 bp mRNA linear PM3-UM0089-170300-002-b07 UM0089 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    South Building, Bath Barel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biology and Biochemistry University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F. Bowen, D. and Blattner, F. A genomic sample sequence of the encompathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence
                                                    Contact: Simpson A.J.G.
                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                           Dias Neto, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is one of 2,122 random reads from the M13 libra annotation of identified clones (BLASTX, BLASTN and
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                                                                                                      sequence tags
                                                                                                                                                                                                                                            Mammalia; Eutheria;
l (bases 1 to 118)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169
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                                                                                      Natl. Acad. Sci. U.S.A. 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size
kb) and then cloned into M13 Janus."
166 c 115 g 143 t
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/clone="PLG00171"
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                                                                                                                                                                                                                          Garcia Correa, R., Verjovski-Almeida, S.,
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1.3e+02;
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Sao Paulo-SP,
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SLCot5F03
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3 CACATGAGTGGCAAGGCGTCTGGTGATA 30
                                                                                                                                                                                                                                                                          University of Georgia
Room 162, Riverbend Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterson,D.G., Schulze,S.R., Sciara,E.B., Lee,S.A., Bowers,J.E., Nagel,A., Jiang,N., Tibbitts,D.C., Wessler,S.R. and Paterson,A.H. Integration of Cot analysis, DNA cloning, and high-throughput
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
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Fax: +55-11-2707001
                                                                                                                                                                                                     Tel: 706-583-0167
Fax: 706-583-0160
                                                                                                                                                                                                                                                                                                                                           Contact: Peterson DG
                                                                                                                                                                                                                                                                                                                                                                                                                sequencing facilitates genome characterization and gene discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.ludwig.org.br/scrip
300-002-b07&t3=2000-03-17&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCATGAGTAGCAAGACGTCTTGTGATA 50
                                                                                                                                                                                                                                                                                                                         ant Genome Mapping Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 149)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence start: 7 quality sequence stop: 76.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                           dgp@arches.uga.edu
Hydroxyapatite-fractionated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inote "Organ: uterus; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
/clone_lib="Sorghum bicolor/tissue_type="leaves"
                                          /organism-"Sorghum bicolor"
/cultivar="BTx623"
/db_xref="taxon:4558"
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor SLCot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_11b-"UM0089"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism≂"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.5%;
85.7%;
                                                                                                                                                                                                                                                                       Research Bldg.,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 97;
                                                                                                                                                                                                                                                                                                                                                                                             (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum bicolor genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                          110 Riverbend Rd.,
                         SLCot!
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pGEM-TA-Easy; A Cot analysis was

performed

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BASE COUNT
ORIGIN
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AUTHORS
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BF676553/c
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCCACATGAGTGGCAAGGCGTCTGGTGATAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence, stop: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602084468F1 NIH_MGC_83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF676553.1 GI:11950448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: CLONETECH Laboratories, cDNA Library Arrayed, by: The I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTCATGCGTAGCACGGCGACTGGTGAGAC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          te: LLCM1067 row: h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases
                                            223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                    (WHELE B = A, C, OF G and N = A, C, G, OF T). Average insert size 1.4 kb (range 0.5-4:0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (PPIO A) TO NOTE TO THE CONTRACT OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI Nr Database. Only the primary match is given (all primar values are < or = 1.00E-5). In no instance does a 'Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing data indicates that each library is representative of the component from which it was derived.
                                                                                                                                                                                                                                                                             sequence:
                                                                                                                                                                                                                                                                                                         note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggccgctteggcc); Site_2: Sfil (ggccattatggcc
); 5' and 3' |adaptors were used in cloning as follows: 5'
adaptor sequence: 5' -CACGGCCATTATGGCC-3' and 3' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sheared genomic DNA.
                                                                                Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:4248641"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to .777)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (T1 phage-resistant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism≈"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          highly-repetitive' (HR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lon/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contain the complete sequence of its putative Nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLCot genomic libraries
                                                                                                                                                                                                                                                                     5;-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.4; DB 1:
Pred. No. 1.3e+02
                                                                            (Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777 bp mRNA linear EST 21-DEC-2000 Homo sapiens cDNA clone IMAGE:4248641 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SL) sequence components from The three repetition-based DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 'moderately-repetitive'
                                                                                CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Based on the resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10\others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae;
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82
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                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                      200-177-g06&t3=2000-02-15&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
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                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ludwig Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.ludwig.org.br/scripts/gethtm
                  GCCACATGAGTGGCAAGGCGTCTGGTGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACATGAGTGGCAAGGCGTCTGGTGA 28
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GCTACATGAGTGCCACGACGTCTTGTGAT 110
                                                                                                                                              58
                                                                                                                                                                                                                                                                                                                                                                      quality sequence start: 32 quality sequence stop: 118.
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   This entry can be seen
                                                                                                                                           stringency conditions
45 c 65 g
                                                                                                                                                                                                                          /note="Organ: breast; Vector: puc18; Site_1: SmaI; Sit SmaI; A mini-library was made by cloning products derifrom ORESTES PCR (U.S. Letters Patent application No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stitute for Cancer Research
Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
1 to 230)
                                                                                                                                                                                                                                                                              /dev_stage="Adult"
                                                                                                                                                                                                                                                                                             clone_lib="BT0615"
                                                                                                                                                                                                                                                                                                         db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                             the pUC 18 vector. Reverse transcription of tiss and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garcia Correa, R., Verjovski-Almeida, S.,
                                                                               63.6%;
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                                                            Score 21; DB 10; I
Pred. No. 2.3e+02;
Pred. No. 5;
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Pred. No. 3.2e+02;
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AV744190 CB
AV744190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
     Email: cgapbb-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Zhu Chen
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
Shanghai Institute of Hematology, Rui-Jin Hospital
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601473642F1 NIH_MGC_68 Homo
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                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       mRNA sequence
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351 Guo Shoujing Road, Zhangjiang Hi- Tech Park,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen, S., Mao, M. and Chen, Z. Homo sapiens CB library cDNA clones Unpublished (2000)
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                                                                                                                                                Unpublished (1999)
                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                     BE784735.1 GI:10205933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 609)
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                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                    numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCACATGAGTGGCAAGGCGTCTGGTGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCATGAGTGCCAAGACGTCTTGTGAT 510
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: 86-21-64740490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript; Site_1: EcoRI; The insert is cloned randomly with the EcoRI digestion" 194\ c 107\ g 141\ t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="cord blood"
/cell_type="CD34+ hematopoletic stem/progenitor cell"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ye,M., Wu,X., Gu,J., Huang,Q.,
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/db_xref="taxon:9606"
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82.8%;
the I.M.A.G.E.
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Pred. No.
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clone CBUAEE04 5', mRNA sequence
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RESULT 11
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UI-R-DKO-cfz-g-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti site and the oligo-dT track served to identify it as a clone from the collection of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                 normalized rat placenta pool library cDNA Lib Soares Lab Clone distribution: clones will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI296816.1
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                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa
451 Eckstein Medical Research Building Iowa City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 538)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                   Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Site_2: SalI; Cloned unidirectionally.
Average insert size 1.8 kb. Library of
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_"Innu_NGC_68"
/clone_tib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-59ORT6;
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DK0
                                                                                                                          /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DKO-cfz-q-01-0-UI"
/clone_lib="UI-R-DKO"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/clone="IMAGE:3876443"
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                                                                                                   dev_stage="ADULT"
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3.8e+02;
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aorta-nRAP

brain-nRBP (20%), heart-nRHP (20%)

, and placenta-nRPP

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                          AV737560 CB Homo sapiens cDNA clone CBUACC11 5', mRNA sequence
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 601)
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                       Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
                                                                                                                                                                                                                                                                                                                                                        AV737560.1 GI:10855141
                                     Shanghai
                                                                                                                                                                Contact: Zhu Chen
                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           milarity :
                                                    is clone is available at Shanghai Hematology Institute in
nese National Human Genome Center at Shanghai
Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong
                                                                                                                                                                                                                               ng,Q., Ye,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                        il: mbshi@ms.stn.sh.cn
                                                                                                            86-21-64740490
                                                                                                                                                                                               sapiens CB library cDNA clones
                                                                                                                                                                                                              ), Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Mao,M. and Chen,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_SEQ=TCACGACAGT"
132 c 142 g
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RESULT 14

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Gaps

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tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOS), heart (CSOS), kidney (CUOS), aorta (CWOS), and placenta (CXOS). The resulting pool of approximately 5,000 clones represented about 33.38 of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of placenta (CXO). The resulting pool of clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA from seven different developmental time points: embryonic day 17, embryonic day 19, embryonic day 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              individually according to the procedure described by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      791-806, 1996). For construction of the DKU subtracted library, plasmid DNA from each of the five individually
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represented about 66.6% of the final driver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lennon & Soares (Genome Research Genome 6:
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536 CTCATGAGTGCCAAGACGTCTTGTGAT 510
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                                               3 CACATGAGTGGCAAGGCGTCTGGTGAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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L Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong
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lone is available at Shanghai Hematology Institute in

    Ye, M., Wu, X., Gu
    Mao, M. and Chen, Z

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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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/lab_host="BM25.8"
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                                                                                                                                                                                                                                                                                                                                                                                                    'clone="CBUAEE03"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens cDNA clone
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85.2%;
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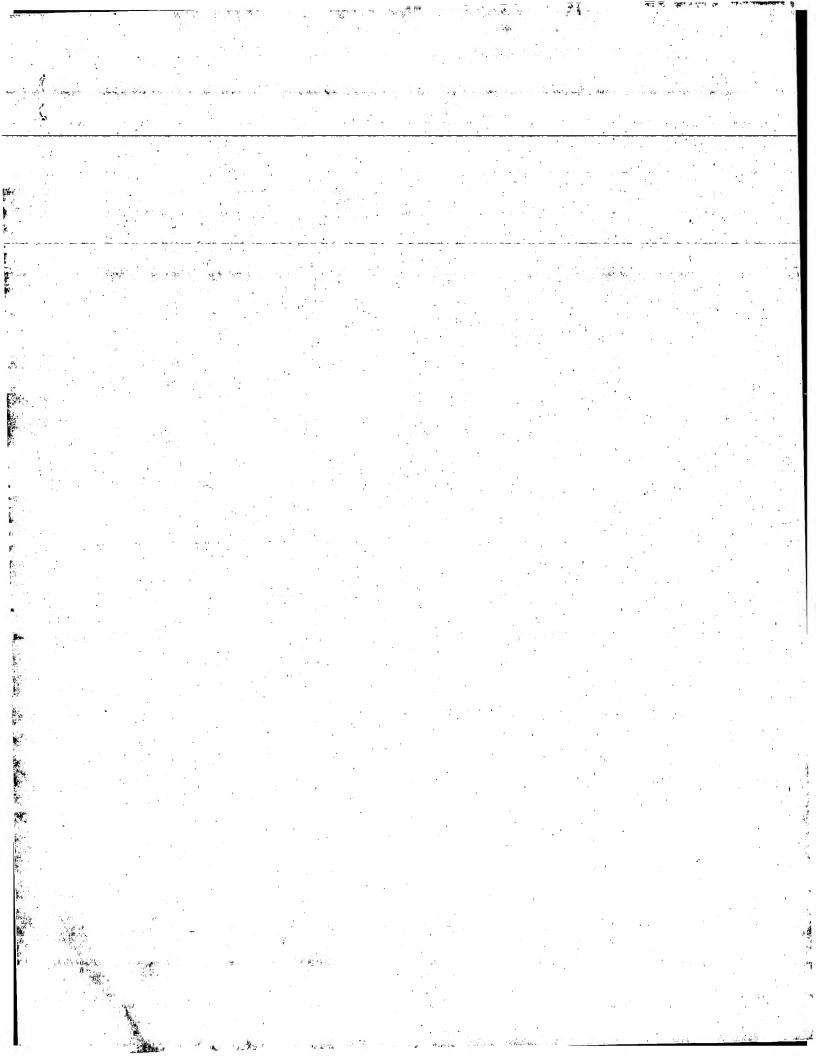
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                                                                                                                                                                                                                                                                               ORGANISM
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| ||||||| |||| ||||| ||||||
36 CTCATGAGTGCCAAGACGTCTTGTGAT 510
                                                                                                                                                                                                                                                                                                                                               PT1.3_04_D05.r tumor1 Homo sapiens cDNA 5', mRNA sequence.
                University of Washington
Department of Molecular Biotechnology, Box 357730,
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
                                                                                                                                        Prostate cancer expression profiling Genomics 59 (2), 178-186 (1999) 99339982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 613)
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AV737831 CB Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 77)
Huang,G.M., Ng,W.1., Farkas,J., He,L., Liang,H.A., G
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                                                                                                                    Contact: Guyang Matthew Huang
                                                                                                                                                                                           and Hood, L
imail: huanggm@yahoo.com
                                                                                                      Leroy Hood
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clone is available at Shanghai Hematology Institute in
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cloned randomly with the EcoRI digestion"
a 194 c 102 g 146 t 3 others
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/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                           CDNA library was constructed using Lambda (Stratagene). mRNA was extracted from a fit tumor tissue (Mayo Clinicg)."
189 c 151 g 146 t 86 others
                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="tumor1"
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Search completed: July 11, 2003, 02:25:43
Job time: 600.333 secs



GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                    Score
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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SS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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SS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
SS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
SS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
SS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gcgdata/geneseq,
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                                                                                                                                                                                                                    IJ
      AAQ14083
AAQ14085
                                              AAV59058
AAH25413
AAL40117
AAL40115
AAS10490
AAZ57775
                                                                                                                                                                             AAT67193
                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /geneseqn-embl/NA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqn-embl/NA2000.DAT:
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Forward PCR primer Pathogenic microor Pathogenic microor Pathogenic microor HCV 5'-UTR domain Hepatitis C virus HCV-T (1-202). HeHCV-KU (1-202). H
                                                                                                                                                                                                                  Description
                                                                                                                                                     Primer ST280A for
                                                                                                                                                                      Hepatitis C virus
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26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26
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24	18	24	21	24	24	24	21	21	21	15	24	24	24	24	18	24	24	19	19	24	19	17	17	17	24	21	24	24	24	19	19	19	14	12	12
ABL46273	AAT77074		AAZ36199	ABK70880	ABK70883	ABK70882	619	AAZ36198	529	9	9	ABN79971	997	ABN79969	AAT87088	ABL46055	ABL46053	AAV70445	AAV70443	ABL46054	AAV70444	AAT29119'	AAT29120	AAT29118	111	777	ABL46061	909	605	045	AAV70450	AAV70449	377	140	AAQ14086
	ש	genome 5'UT	pted HCV 5' no	genome 5'UTR	genome 5'UTR	genome	HCV 5'	ted HCV 5' I	epati	is C vir	itis C	itis C	isc	atitis C	fic	is C	atitis C vir	subtype 20	nsu	atitis C	type	is c	ი	ဂ	S C	C	ი	ဂ	atitis C vir	subtype 2c	subtype 1b	ubtype la	ned HCV 5' no	-I (1-202).	HCV-N (1-200). He

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## ALIGNMENTS

TIG.	AAT67193
ž H	AAT67193 standard; DNA; 26 BP.
	AAT67193;
	13-FEB-1998 (first entry)
	Hepatitis C virus (HCV) RNA amplification primer ST280A.
	e de la comoca y de comoca y d
	Synthetic.
	EP776981-A2.
	04-JUN-1997.
	21-NOV-1996; 96EP-0118704.
	20-NOV-1005: 05178-0007730
	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
	Tsang SY;
	WPI; 1997-291296/27.
	Oligonucleotide primers for hepatitis C virus $\ensuremath{RNA}$ amplification by polymerase chain reaction

Claim

Page 11;

l6pp; English.

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RESULT 2
AAV59058
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                                                                                           This sequence represents a primer for a fragment of HCV, and is an example of an oligonucleotide of the invention. The oligonucleotides of the invention are of the formula 5'-S1-Nu-3' or 5'-S1-Nu-S2-3', where nucleotides; and Nu is a nucleotides; S2 is a sequence of 1-3 nucleotide with a purime or pyrimidine base having an exocyclic amino group substituted by CHRIR2; R1, R2 are H, substituted naphthyl. The oligonucleotides are useful as primers for
              nucleic acid amplification, preferably by polymerase chain reaction. Use of the modified primers reduces non-specific amplification, especially primer dimer formation, with a concomitant increase in the yield of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                    Oligo-nucleotide(s) containing N-substituted nucleotide - primers for nucleic acid amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-482929/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP866071-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer; HCV; nucleic acid amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C.virus (HCV) RNA by reverse compility a 250 base pair product from the 5' untranslated region of the HCV genome. This can be used to detect HCV in a sample with increased sensitivity. Amplification of HCV nucleic acid using this primer is up to the companion of the primer is the contract of the contract of the primer is up to the contract of the contract of the primer is up to the contract of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                               6; Page 16; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ST280A for HCV fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOFFMANN LA ROCHE & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young KKY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGAAAGCGTCTAGCCATGGCGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0041127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98EP-0104461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "optionally benzylated, methylated, or nitrobenzylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 G; 5 T; 0 other;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS
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RESULT 4 AAL40117 ID AAL4

AAL40117 standard;

DNA;

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GCAGAAAGCGTCTAGCCATGGCGTTA GCAGAAAGCGTCTAGCCATGGCGTTA

26 26 Matches

26;

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AAH25413
         Query Match
Best Local
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Best Local
                                                  The specification describes a composition of magnetic glass particles, which contain at least one magnetic object with a mean diameter between 5-500 nm. The composition is useful for the purification of nucleic acids. The composition can be used to process large quantities of nucleic acid samples, because it does not involve the particles being centrifuged or the fluids being drawn through glass fiber filters. PCR primers AAH25413-14 were used to amplify HCV DNA fragments. The amplified fragment can be purified using the method of the invention.
                                     Sequence 26 BP; 7 A; 6 C; 8 G;
                                                                                                                                                                                                                                                                                                           17-NOV-1999;
12-MAY-2000;
                                                                                                                                                                 Example 7; Page 98; 105pp; English
                                                                                                                                                                                                   or RNA
                                                                                                                                                                                                                 Novel
                                                                                                                                                                                                                                     WPI; 2001-381247/40
                                                                                                                                                                                                                                                             Weindel K,
                                                                                                                                                                                                                                                                                                                                           17-NOV-2000; 2000WO-EP11459
                                                                                                                                                                                                                                                                               (HOFF ) ROCHE DIAGNOSTICS GMBH
                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                               WO200137291-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Magnetic glass particle; nucleic acid purification; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forward PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-2001
       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH25413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH25413 standard;
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                                                                                                                                                                                            composition of magnetic glass particles A in automated processes
      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGAAAGCGTCTAGCCATGGCGTTA 26
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                                                                                                                                                                                                                                                           Riedling M,
                                                                                                                                                                                                                                                                                                          99EP-0122853.
2000EP-0110165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifier:
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to amplify a HCV DNA fragment.
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               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 C;
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                                                                                                                                                                                                                                                                                                                                                                                                          "derivatisation with a p-(t-butyl)benzyl-residue"
                                                                                                                                                                                                                                                         Geiger
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Score
Pred.
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                                       5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
  26;
No.
                                   0 other;
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                                                                                                                                                                                                    for purification
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          26;
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RESULT 5
AAL40115
ID AAL4
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                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                                                                                                                                                                                                                                  The invention relates to a probe containing a 410 or 20 base pair sequence, given in the specification. It is capable of detecting the tuberculosis bacterial group including Mycobacterium tuberculosis, Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti and/or Mycobacterium canotti. The method is useful in disease diagnosis and monitoring therapy. This polynucleotide sequence represents a probe
                                                                                   Tuberculosis; Mycobacterium; bovis; BCG; africanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2000; 2000JP-0396222
26-DEC-2000; 2000JP-0396321
29-JUN-2001; 2001JP-0199552
13-SEP-2001; 2001JP-0278920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monitoring therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis; Mycobacterium; bovis; BCG; africanum; microti; canotti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2002
                   04-JUL-2002
                                                         Unidentified
                                                                           monitoring therapy;
                                                                                                    Pathogenic microorganism detecting PCR primer SEQ ID No 41.
                                                                                                                          13-SEP-2002
                                                                                                                                             AAL40115;
                                                                                                                                                              AAL40115 standard;
                                                                                                                                                                                                                                                                                       Sequence 53 BP; 12 A; 13 C; 17 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                      Claim 57;
                                                                                                                                                                                                                                                                                                                                                                                                      Detecting pathogenic microorganisms with oligonucleotide primers, useful in disease diagnosis and monitoring thera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200252043-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pathogenic microorganism detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL40117;
26-DEC-2001; 2001WO-JP11422
                                       WO200252043-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-500769/53.
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                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                             GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                            GCAGAAAGCGTCTAGCCATGGCGTTA
                                                                                                                                                                                                                                                                                                                                                                                    Page 98; 106pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hino F,
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-JP11422
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                                                                                                                          (first
                                                                                                                                                                                                                                                                                                           detection of
                                                                                                                                                              DNA;
                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogenic microorganism; probe; ss.
                                                                           pathogenic microorganism;
                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kato I;
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                                                                                                                                                                                                                                                                                                           pathogenic microorganisms
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Pred.
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No.
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                                                                                                                                                                                                                                                                     Length 53;
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                                                                           primer;
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                                                                                 microti; canotti;
                                                                                                                                                                                                                                                                                                                                                                                                      therapy
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                                                                                                                                                                                                                                                                                                           invention
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Best Local S
Matches 26
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26-DEC-2000;
29-JUN-2001;
misc_binding
                                     misc_binding
                                                                                                    misc_binding
                                                                                                                                                                                                                                                            HCV 5'-UTR
                                                                                                                                                                                                                                                                                                                   AAS10490 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                stem_loop
                                                                                                                               stem_loop
                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                               24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
73..77
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The invention relates to a probe containing a 410 or 20 base pair sequence, given in the specification. It is capable of detecting the tuberculosis bacterial group including Mycobacterium tuberculosis, Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti and/or Mycobacterium canotti. The method is useful in disease diagnosis and monitoring therapy. This polynucleotide sequence represents a PCR primer relating to the detection of pathogenic microorganisms of the
                                                                                                                                                                                                                                                                                                   HCV 5'-UTR; minimal IRES; mIRES; internal ribosome entry site; eIF3; eukaryotic initiation factor 3; HCV translation initiation; antivira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting pathogenic microorganisms with oligonucleotide probes and primers, useful in disease diagnosis and monitoring therapy
                                                                                                                                                                                                                                                              Hepatitis Č virus strain Ia
                                                                                                                                                                                                                                                                                       RNA electrophoretic gel mobility shift assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hino F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000JP-0396222.
; 2000JP-0396321.
; 2001JP-0199552.
; 2001JP-0278920.
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                                      /*tag=
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55..60
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23..28
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                                                                            32..50
            /bound_moiety=
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Pred.
"Forms double bases 28-23"
                                                                                                                                                                                  "Forms double stranded bases 73-77"
                                                                                         "Forms double
bases 60-55"
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                                                    as
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No.
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The present sequence represents Hepatitis C virus (HCV) 5'-UTR domain II RNA probe used in a RNA electrophoretic gel mobility shift assay (EMSA). The present sequence is described in an cinvention relating to a novel compound comprising nucleotide sequences crapable of annealing and which is derived from a 5'-untranslated crapable of entry of HCV which is essential for binding of eIF3 (eukaryotic cinitiation factor 3). The invention particularly relates to a cribosome entry site (mIRES) which can be used to identify drugs which contained the compounds of the invention may contain the mIRES enable potential HCV antiviral compounds. Assays based con the mIRES enable potential antivirals to be screened in a cheaper compound are suitable to parallel processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
                         10-MAY-1994;
                                                                                                                      Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ssanti-inflammatory; translation inhibition; HCV infection; virucide.
                                             07-JUN-1995;
                                                                                         US6001990-A.
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AAZ57775
                                                                                                               Hepatitis
                                                                                                                                                                     Hepatitis
                                                                                                                                                                                         05-APR-2000
                                                                                                                                                                                                               AAZ57775
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5E; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequences derived from Hepatitis C virus, useful for identifying candidate antiviral compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-465050/50
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22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                standard;
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                                                                                                              C virus
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                                                                                                                                                               virus antisense
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                      94US-0240382.
                                            95US-0474700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99GB-0029820
99US-0171804
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/bound_moiety=
                                                                                                                                                                                                                              DNA; 155
                                                                                                                                                                                                                                                                                                                                          80.8%;
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                                                                                                                                                          inhibitor oligonucleotide #41.
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Sequence 155 BP;
                       virucide, hepatotropic and anti-inflammatory activity, and are useful treating HCV infection by inhibiting translation of type I-V HCV RNA. Hepatitis C virus is a positive strand RNA virus, and is the major causative agent of post-transfusion hepatitis. Persistent HCV infection lead to chronic hepatitis, cirrhosis, and hepatocellular carcinome
                                                                                                 This sequence is an uncountry physiological conditions. The Hepatitis C virus (HCV) RNA, under physiological conditions. The invention relates to HCV antisense oligonucleotides, and also for a vector comprising a nucleotide sequence which is transcribed in an animal cell to generate an antisense oligonucleotide. The oligonucleotides have
                                                                                                                                                                                   This sequence is an antisense oligonucleotide Hepatitis C virus (HCV) RNA, under physiologic
                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                             Antisense oligonucleotide to Hepatitis Hepatitis C virus infections -
                                                                                                                                                                                                                                                                                                                                                                            Moradpour
                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                         2000-104900/09
   29 A; 43 C;
                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                        31pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Wakita
51 G;
                                                                                                                                                                                                                                                                                                                                                                        H
 32 T;
                                                                                                                                                                                                                                                                                     C virus RNA, useful for treating
0 other;
                           and hepatocellular carcinoma.
                                              is the major
ent HCV infection
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RESULT 8
AAQ14083
                                                                                                                                                                                            Matches
Hepatitis C virus
                Epitope; PCR; diagnosis;
                                     HCV-T (1-202)
                                                           03-JAN-1992
                                                                               AAQ14083;
                                                                                                                                                88 GCAGAAAGCGTCTAGCCATGGCGTTA
                                                                                                                                                                  1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                          l Similarity
26; Conserv
                                                                                                 standard; DNA; 202
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Pred. No.
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Query Match Best Local (

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Length 155;

Gaps

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Disclosure; Fig 1(I); New nucleotide sequences of hepatitis C virus infe

79pp;

Japanese

infection

encoding HCV epitope(s) - fection via polymerase chain

for diagnosis n reaction

The nucleotide sequences represented in AAQ14076-86 and AAQ14767-71 encode epitopes from structural, non-structural and 5' untranslated domains of hepatitis C virus. The sequences are used for accurate and simple diagnosis and typing of HCV infection, using PCR

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Takada T,

Enomoto N,

Date T,

Nakao

Η,

(MITK ) MITSUI TOATSU

CHEM INC.

09-NOV-1990; 28-MAR-1990; 13-JUN-1990; 14-JUN-1990;

90JP-0305795. 90JP-0080185. 90JP-0154230. 90JP-0153979.

91WO-JP00405

PD XX PF

03-OCT-1991. 28-MAR-1991;

WO9114779-A

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RESULT 10
AAQ14086
ID AAQ14
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AC AAQ14
XX
DT 03-JA
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28-MAR-1990;
13-JUN-1990;
14-JUN-1990;
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03-JAN-1992
                    AAQ14086;
                                                                                                                                                                Sequence 202 BP;
                                                                                                                                                                                   amplification
                                                                                                                                                                                                                                                           New nucleotide sequences encoding HCV epitope(s) - for diagnosis of hepatitis C virus infection via polymerase chain reaction
                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus
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                                      AAQ14086 standard; DNA; 202
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90JP-0080185.
90JP-0154230.
90JP-0153979.
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Pred. No. 0.0032;
Mismatches 0
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RESULT 11
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                         .09-NOV-1990;
28-MAR-1990;
13-JUN-1990;
14-JUN-1990;
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28-MAR-1990;
13-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The nucleotide sequences represented in AAQ14076-86 and AAQ14767-71 encode epitopes from structural, non-structural and 5' untranslated domains of hepatitis C virus. The sequences are used for accurate and simple diagnosis and typing of HCV infection, using PCR
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                                                                                                 28-MAR-1991;
                                                                                                                            03-OCT-1991
                                                                                                                                                       WO9114779-A
                                                                                                                                                                             Hepatitis C virus.
                                                                                                                                                                                                              Epitope; PCR;
                                                                                                                                                                                                                                       HCV-I (1-202).
                                                                                                                                                                                                                                                                     03-JAN-1992
                                                                                                                                                                                                                                                                                               AAQ14084;
                                                                                                                                                                                                                                                                                                                          AAQ14084 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 202 BP; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1(I); 79pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequences encoding HCV epitope(s) - f of hepatitis C virus infection via polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-310579/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9114779-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCV-N (1-200).
(MITK ) MITSUI TOATSU CHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplification techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITK ) MITSUI TOATSU CHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                Ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enomoto N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                        90JP-0305795.
90JP-0080185.
90JP-0154230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90JP-0305795.
90JP-0080185.
90JP-0154230.
90JP-0153979.
                                                                                                91WO-JP00405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91WO-JP00405
                          90JP-0153979
                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; 60 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date T,
                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                           ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DE Pred. No. 0.0 ... DE Pred. No. 0.0 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakao T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 202;
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Best Local
                                               region a pair of oligonucleotioes was well as primers for HCV PCR. HCV RNA was isolated from HC-JI were used as primers for HCV PCR. HCV RNA was isolated from serum of a putatively infected individual. RNA reverse transcription PCR was performed and a specific PCR prod. identified. The prod. was used to transform E. coli DH5 alpha to obtain pGHCVIA contg. a 342 bp insertion from the HCV 5' non-coding region. This probe is highly specific and sensitive for HCV RNA. The probe can be shighly specific and sensitive for HCV RNA. The probe can be shighly specific and sensitive for HCV RNA. The probe can be shighly specific and sensitive for HCV IN samples, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                         disease, to
                          be used to quantitively detect the amt. of HCV in samples, to analyse the molecular forms of HCV RNA during evolution of the disease, to localise HCV in hepatic and/or extrahepatic tissues
                                                                                                                                                                                                                     Claim 1; Fig 4; 26pp;
                                                                                                                                                                                               To obtain
                                                                                                                                                                                                                                                                        Detection
                                                                                                                                                                                                                                                                                                                                 Hu K,
                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                               (CEDA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP531974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; probe; hepatocellular necrosis; hepatocellular; carcinoma; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ3777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The nucleotide sequences represented in AAQ14076-86 and AAQ14767-71 encode epitopes from structural, non-structural and 5' untranslated domains of hepatitis C virus. The sequences are used for accurate and simple diagnosis and typing of HCV infection, using PCR amplification techniques:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ37774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1(I); 79pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequences encoding HCV epitope(s) - for diagnosis of hepatitis C virus infection via polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takada
                                                                                                                                                                                                                                                                                                1993-087007/11.
                                                                                                                                                                                                                                                      derived
                                                                                                                                                                                                                                                                                                                               Vierling JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV 5' non coding region from pGHCV1A.
           and hepatocellular co
                                                                                                                                                                                                                                                                                                                                                          CEDARS SINAI MEDICAL
                                                                                                                                                                   HCV cDNA nucleotide sequences from the 5' non-coding pair of oligonucleotides based on the reported sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                   of hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGAAAGCGTCTAGCCATGGCGTTA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 BP; 41 A; 60 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enomoto N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                        91US-0758862
                                                                                                                                                                                                                                                  from the 5'-non-coding
                                                                                                                                                                                                                                                                                                                                                                                                                   92EP-0115426
                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                              virus (HCV) RNA - using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
between HCV infection, hepatocellular arcinoma. The probe can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakao
                                                                                                                                                                                                                                                region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0032
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                                                                                                                                                                                                                                             the HCV genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                               genome
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AAV70449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSXSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                             I probe complementary to at least 1 single stranded region; and (11) at least 1 probe complementary to at least a portion of the folded target; and (b) mixing the target and probes so that the probe hybridises to form a probe /folded target complex. Also provided are methods for determination of structure formation in nucleic acid targets; for analysing folded methods can be used for the detection and characterisation of nucleic acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles of mammalian manes associated with discourse research to the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles
                                                                                                                                                                                                                                                   The invention relates to methods and compositions of detection and characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (a) providing: (i) a folded target having a DNA sequence comprising at least 1 double stranded region and at least 1 single stranded region; and (ii) at least
                                                                                                                                                                                                                                                                                                                                                                                    Detection and characterisation of nucleic acid sequences - by a folded target and one or more probes to form a probe/folded complex and detecting and characterising the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1998;
05-MAY-1997;
19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 169; 279pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson TA,
Lyamichev VI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9850403-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (THIR-) THIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid detection; nucleic acid characterisation; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV subtype la PCR fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnose HCV infection,
anti-HCV therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 242 BP; 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brow MAD,
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97US-0851588.
97US-0934097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP,
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100.0%; Pred. No. 0:1
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prudent JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ť
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forensic; paternity; multiplexing; HCV; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67· G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242;
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                                                                                                                                                                                                                                                                                                                                                                                                     mixing
.target
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of mammalian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous analysis of both strands (e.g. the sense and antisense strands) and are ideal for high-level multiplexing. The products produced are amenable to qualitative, quantitative and positional analysis. The methods may be performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer

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RESULT 14
AAV70450
ID AAV70
XX AV70
XX O8-AI
DT 08-AI
CX Nucli
KW Nucli
KW infec
XX Hepat
XX Hepat
XX Hosel
PN WO98:
XX 12-NC
XX 05-MJ
PR 03-MJ
PR 03-MJ
PR 19-SE
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    method of detection and characterisation comprises: (a) providing: (i) a control of detection and characterisation comprises: (a) providing: (i) a control of the folded target having a DNA sequence comprising at least 1 double complementary to at least 1 single stranded region; and (ii) at least control of the folded target; and control of structure formation in nucleic acid target; for analysing folded control of a control of a control of control control control control of control of control of control contr
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Best Local
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05-MAY-1997;
19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection and characterisation of nucleic acid sequences - by a folded target and one or more probes to form a probe/folded complex and detecting and characterising the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson TA,
Lyamichev VI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid detection; nucleic acid characterisation; hybridisation; infection; disease; cancer; forensic; paternity; multiplexing; HCV; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCV subtype 1b
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                                                                                                                                                                                                                                                                                                                                                                                 characterisation
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to methods and compositions of detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9850403-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3;
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Neri BP,
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97US-0934097.
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Best Local
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The methods are powerful in that they allow for analysis of longer
fragments of nucleic acid than current methodologies. Sequences
AAV/0449-52 represent a hepatitis C virus (HCV) subtype sequences
produced by PCR. These PCR products can be used in hybridisation an
using multiple capture probes for HCV genotyping.
                                                                                                                                                       HCV subtype
                                                                                                                              Nucleic acid detection; nucleic acid characterisation; hybridisation;
                                                                                                                                                                                   08-APR-1999
                                                                                                                                                                                                             AAV70451
                                                                                                                                                                                                                                      AAV70451 standard; DNA; 244
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 244 BP;
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Anderson TA, I 03-MAR-1998; 05-MAY-1997; (THIR-) THIRD 19-SEP-1997; 05-MAY-1998; WO9850403-A1 12-NOV-1998 Brow MAD, Neri BP, WAVE TECHNOLOGIES 98US-0034205. 97US-0851588. 97US-0934097. 98WO-US03194 Dahlberg JE, Prudent JR; Dong Ę Fors ŗ

Hepatitis C virus. infection; disease;

cancer;

forensic;

paternity; multiplexing;

HCV;

gp

Detection and characterisation of nucleic acid sequences - by a folded target and one or more probes to form a probe/folded complex and detecting and characterising the complexes

mixing target

WPI; 1998-610317/51.

3; Page 169; 279pp; English.

probe /folded target complex. Also provided are methods for determination of structure formation in nucleic acid targets; for analysing folded nucleic acids targets; and for analysis of nucleic acid structures. The methods can be used for the detection and characterisation of nucleic acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (a) providing: (i) a folded target having a DNA sequence comprising at least 1 double stranded region and at least 1 single stranded region; and (ii) at least 1 probe complementary to at least a portion of the folded target; and (b) mixing the target and probes so that the probe hybridises to form a identification of the source of nucleic acids found in forensic samples as well as in paternity determinations. The methods allow simultaneous analysis of both strands (e.g. the sense and antisense strands) and are as well as of mammalian genes associated with disease and cancers, The invention relates to methods and compositions of detection and the and

Search completed: July 10, 2003, 19:52:41 Job time: 56.8629 secs	Qy 1 GCAGAAAGCGTCTAGCCATGGCGTTA 26	Query Match 100.0%; Score 26; DB 19; Length 244; Best Local Similarity 100.0%; Pred. No. 0.0033; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SQ Sequence 244 BP; 46 A; 68 C; 78 G; 52 T; 0 other;	CC produced by PCR. These PCR products can be used in hybridisation analysis CC using multiple capture probes for HCV genotyping.	CC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of the CCC AAV70449-52 represent a hanatitie of virus (TOV) subtrue common of virus (TOV)	CC performed in solution or in the solution phase (e.g. on a solid support).  CC The methods are newsful in that the collection of the solution of the solution phase (e.g. on a solid support).	CC ideal for high-level multiplexing. The products produced are amenable to
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	US-08-851-588-21	US-08-934-097A-21	US-09-034-205-21	US-08-520-946-130	US-08-520-946-124	US-08-757-653-130	US-08-757-653-124	US-08-520-946-131	US-08-520-946-129	US-08-520-946-128	US-08-520-946-125	US-08-520-946-123	US-08-757-653-131	US-08-757-653-129	US-08-757-653-128	US-08-757-653-125	US-08-757-653-123	US-08-474-700B-40
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## ALIGNMENTS

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Sequence 1, Application US/08738928
Patent No. 5837442
GENERAL INFORMATION:
                                                                                                                                                                                                                                 TELEFAX: (510) 814-297 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PELTY, DOUGLAS A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Olic
TITLE OF INVENTION: HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/738,928 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                              STRANDEDNESS:
1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Hoffmann-La Roche Inc.
340 Kingsland Street
                                                                                                                                                                                                                                               (510) 814-2974
(510) 814-2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                             Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
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SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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Matches
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NAME: Petry, Douglas A
REGISTRATION NUMBER: 35,321
                                                                                                                                                               DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                   OF SEQUENCES:
                APPLICATION DATA:
                                                                    TYPE: 3.5" Diskette,
                                                                                                                                    Boston
                                                                                                                                                                     NDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                           001990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARE: Patentin Rel
APPLICATION DATA:
                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                              ORMATION:
                                                                                                                                                                                                                                                                                                                                            GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                    GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Branchburg
                                                                                                                                                                                                                                                                                  Application US/08474700B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     READABLE FORM:
TYPE: Floppy dis)
                                                                                                                                           225 Franklin Street
                                                                                                                                                                                                                     Moradpour, Darius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATION:
                                                                                                                                                                                                                                Wakita, Takaji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09039866
                                         IBM PS/2 Model 50z or 55sx
SYSTEM: MS-DOS (Version 5.
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                    Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roche Molecular Systems 1080 U.S. Highway 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
.07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
      US/08/474,700B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                          Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-634-797-44
  Query Match
Best Local Similarity
                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 1226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510,601-3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                  NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFORMATION FOR SEQ ID NO:
                                                                            STRANDEDNESS:
                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER OF SEQUENCES:
                                                                                                       LENGTH:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 19-APR-1996
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                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00
FELECOMMUNICATION INFORMATION: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          RRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                                                                                              94608-2916
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 155 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                           4560 Horton Street - R440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08634797
                                                                                                                                                      (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                          PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                        IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                        Chiron Corporation
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                                                   DNA (genomic)
                                                                             single
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 100.0%;
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Score 26; DB 2;
Pred. No. 0.00086;
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                                                                                                                                                                                                                                                                                          Version #1.30
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Length 194;

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                                                                                                                                                                                          quence 46,
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                                                                                                                                                         ENERAL INFORMATION:
                                                                                                                                                                         ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMANDED.
                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 12
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
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                                                                            ORRESPONDENCE ADDRESS:
                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Harbin, Alisa A. REGISTRATION NUMBER: 33,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 19-APR-1996 CLASSIFICATION: 435
COUNTRY:
                                                             DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 45, 5.
5851759
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                                                                                                                                                                           b, Application US/08634797
5851759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                      GCAGAAAGCGTCTAGCCATGGCGTTA 26
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             California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Chiron Corporation
4560 Horton Street - R440
                                           2: Chiron Corporation
4560 Horton Street - R440
                                                                                                                                          WEINER, AMY J:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     ·linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (510) 601-3274
                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                             GENOTYPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOTYPING
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                                                                                                          HETERODUPLEX TRACKING ASSAY (HTA) FOR GENOTYPING HCV
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                                                                                                                                                                                                                                                                                                                                   Score 26; DB 2;
Pred. No. 0.00086;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                    Gaps
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Patent No. 5851759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Harbin, Alisa A.

REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 1226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-3274
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SENERAL INFORMATION:
                          NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                          REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
                                                                         TELEFAX:
                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                          NAME: Harbin, Alisa A. REGISTRATION NUMBER:
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/634,797 FILING DATE: 19-APR-1996
                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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94608-2916
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                                                                            (510)
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                                                                                             (510)
                                                                              655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HETERODUPLEX TRACKING ASSAY (HTA) FOR GENOTYPING HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                    Release #1.0,
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                                                                                                                                          33,895
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Length 194; Indels

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Gaps

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RESULT 9
US-08-634-797-50
                                          Sequence 50,
Patent No. 5
GENERAL INFO
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Best Local
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    TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No. 58
ENERAL INFO
                                                                                                                                                                                                                                                                                                                                                                                            NAME: | Harbin, Alisa A;
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19-AP
                                       INFORMATION:
                                                                                                                                                                                                             Similarity
 INVENTION:
                                                                                                                                                                                                                                                                                                                                    N/A
N FOR SEQ ID NO:
CHARACTERISTICS:
                                                                                                                                    GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                           194 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENT INFORMATION:
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                                                                     Application US/08634797
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[CATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4560 Horton Street - R440
                            WEINER, AMY J.
                                                                                                                                                                                                                                                                                                                                                                                  (510)
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ilarity 100:0%;
Conservative
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HETERODUPLEX TRACKING ASSAY (HTA) FOR GENOTYPING HCV
                                                                                                                                                                                                          100.0%; Score 26; DB 2; 100.0%; Pred. No. 0.00086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HETERODUPLEX TRACKING ASSAY (HTA) FOR
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Pred. No.
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Matches
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Best Local 9
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                           ZIP: .94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION:
                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A
                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,797
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
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                NAME: Harbin, Alisa A. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: .Floppy disk
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4560 Horton Street - R440
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                                                                                                                                                                                                                                                                                                                    Chiron Corporation
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HETERODUPLEX TRACKING ASSAY (HTA) FOR
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                                                                                                            US/08/634,797
                          33,895
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              1226.001
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                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: HATAIN, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 1226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 52,
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                                                                                                                                                                                                              NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 194 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 194 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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5851759
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                        GCAGAAAGCGTCTAGCCATGGCGTTA 26
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GCAGAAAGCGTCTAGCCATGGCGTTA 26
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(510) 655-3542
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                                                                                                                                           linear
                                                                                                                        DNA (genomic)
                                                                                                                                                     single
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Pred. No.
                                                                   Score 26;
Pred. No.
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                                                      Mismatches
                                                                 DB 2; 1
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                                                                               Length 194;
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                                                    Indels
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RESULT 12

COUNTRY:

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Matches
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                                                                                                                                                                                                             atent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,595
FILING DATE: 08-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 611 ....
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                        TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100 les 26; Conservative
                                                  STREET:
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                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/758,862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                   San Francisco
CA
USA
                                                                                                                                                                                                                                                                                                                          GCAGAAAGCGTCTAGCCATGGCGTTA 26
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                                                                                                                                                                                                                          Application US/09034205
                                                 220 Montgomery Street, Suite 2200
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                                                                                                                                    Neri, Bruce P.
                                                                                                                                              Brow, Mary Ann D. Fors, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIERLING, JOHN M
                                                                                                                                                                                 Lyamichev, Victor I.
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SYSTEM: PC-DOS/MS-DOS
                                                                MEDLEN & CARROLL,
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Pred. No.
                                                                , LLP
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                   0.00089
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TYPE:

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APPLIC.
APPLICATION:
ETILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, Kamrin T;
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-03268
REFERENCE/OCKET NUMBER: FORS-03268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEPHONE: (415) 397-8338
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Best Local
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 base pairs
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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DESCRIPTION: /desc = "DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING OLIGONUCLEOTIDES
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STRANDEDNESS: double
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220 Montgomery Street, Suite 2200
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,23
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                                                                                                       TOPOLOGY:
                                                                                                                  STRANDEDNESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FR: FORS-03268
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1 US-09-825-574-26
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US-09-940-925A-131
US-09-941-193A-125
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Sequence 27, P
Sequence 28, P
Sequence 123, P
Sequence 125, P
Sequence 128, P
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7, Appl
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  RESULT 2
US-10-029-907-17
Sequence 17, Application US/10029907
Patent No. US20020142350A1
GENERAL INFORMATION:
APPLICANT: BOBEHRINGER INGELHEIM (CANADA) LTI
APPLICANT: OF INVENTION: SELF REPLICATING RNA MOI
TITLE OF INVENTION: HEPATITIS C VIRUS
FILE REFERENCE: 13/083
CURRENT APPLICATION NUMBER: US/10/029,907
CURRENT FILING DATE: 2001-12-21
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LENGTH: 26
TYPE: DNA
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Publication No. US20030054372A1
GENERAL INFORMATION:
APPLICANT: JAEGER, STEPHAN
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Best Local
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CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A METHOD FOR TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
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llarity 100.0%;
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0 US-09-345-761-7
0 US-09-914-357-3
US-10-259-275-25
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Sequence 27, App11
Sequence 37, App11
Sequence 38, App1
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                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A METHOD TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999
            OTHER INFORMATION: Description OTHER INFORMATION: QS HCV (HCV OTHER INFORMATION: and ST2535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/1:
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
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                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-087-631¤-13
                                                                                                                                             ORGANISM:
                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                     Q ID NO 13
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: DNA SOTHER INFORMATION: amplification of HCV type 1 using primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPPLICANT: JAEGER, STEPHAN
TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING CONTROL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LO-087-631B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                                                                                                                                                                                                                                                              PatentIn
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                                                                                                                                Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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ilarity 100.08;
Conservative
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                                                                                                                                                                                                                                                    version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STEPHAN
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                                                                                                                                                                                                                                                                                                                                                                                                                 FOR THE DETERMINATION OF A NUCLEIC ACID USING A
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      n of artificial:
V amplification
) using primers
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Pred. No. 0.0027;
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Pred. No.
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            control
ST280 an
                                                                 sequence:
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      nce: Amplicon sequence derived for having binding sites for ST280 and ST778
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imers ST280 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
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Patent No. US20020119454A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999 CURRENT APPLICATION NUMBER: US/10/087,631B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-03-01 NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                 CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION
                                                    PRIOR
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
Structure Probing With Structure-Bridging
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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26; Conserv
                                                            APPLICATION NUMBER: US/09/825,574
FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>
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                 APPLICATION DATA:
APPLICATION NUMBER: 08/934,097
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGAAAGCGTCTAGCCATGGCGTTA 26
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                                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                                                                                                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                           STREET: 220 Montgomery Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                             ADDRESSEE: MEDLEN & CARROLL,
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                                                                                                                                                                                                                                                                                                                                                                                                                               Brow, Mary Ann D.
                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                Bruce P.
                                                                                                                                                                                                                                                                                                                                                                                                                Lance
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                                                                                                                                                                                                                                                                                                                                              Oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Victor I.
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0;
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Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                             LLP
                                                                                                                                                                                                                                                                           Suite
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                                                                                                                               Version #1.30
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REFERENCE/DOCKET NUMBER:

FORS-02980

NUMBER: 38,230

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US-09-825-574-27; Sequence 27, A
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Best Local Similarity
Matches 26; Conserv
                                                      INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 base pairs
TYPE: nucleic acid
STRRNDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       squence 27, Application US/09825574 stent No. US20020119454A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/825,574
FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
Structure Probing With Structure-Bridging
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Brow, Mary Ann D.
Fors, Lance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/934,097 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)
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                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
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TYPE: other nucleic acid 
RIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neri, Bruce P.
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ON: /desc = "DNA"
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                                                                                                                                       US-09-825-574-28
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Best Local
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                                                                    Matches
                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                              TELEFAX: (415) 39
INFORMATION FOR SEQ ID NO:
                                                                                     Local
                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/934,097
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lyamichev, Victor I.
Brow, Mary Ann D.
Fors, Lance
                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
Structure Probing With Structure-Bridging
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                                  1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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                                                                                     Similarity.
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CAGAAAGCGTCTAGCCATGGCGTTA 26
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FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                            LENGTH: 244 base pairs
                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 705-8410
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s20020119454A1
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                                                                   100.0%; Score 26; DI
100.0%; Pred. No. 0.0
tive 0; Mismatches
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Pred. No. (
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                                                                                                         DB 10;
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                                                                                                     Length 244;
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                                                                   Indels
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RESULT 9 US-09-940-925A-123

Sequence 123, Application US/09940925A

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RESULT 10
US-09-940-925A-125
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SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-09-940-925A-123
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Best Local
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     lication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lication No. US200300543381
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO:
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                        APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MEDLEN & CARROLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGAAAGCGTCTAGCCATGGCGTTA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                        COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 281 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/940, 925A FILING DATE: 10-Jun-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
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5. US20030054338A1
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ilarity 100.0%;
Conservative
                                                                               94104
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                                                                                                                                                                                                                       PATHOGENS
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Pred. No. 0.0027
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                                                                                                                                         SUITE 2200
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Query Match
Best Local Similarity
""" hes 26; Conserve
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                                                                                                       INFORMATION FOR SEQ ID NO: 128: SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uence 128, A
lication No.
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 128:
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin R
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 125:
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APPLICATION NUMBER: US/09/940,925A
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                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              TELEFAX:
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                              NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
                                          POPOLOGY:
                                                                                      LENGTH: 281 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 220 MONTGOMERY STREET, CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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D. US20030054338A1
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                                                                                                                                            (415)
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                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                    linear
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                                                                                                                                            397-8338
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Pred. No. 0.0027;
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                                                                                                                                                                                              FORS-01756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUITE 2200
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US-09-940-925A-128

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                                                                                                                                 US-09-940-925A-131/c
                                                                            Sequence 131, Applicate Publication No. US200: GENERAL INFORMATION
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                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIVE, DAVID M. TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATION FOR SEQ ID NO: 129
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      271 GCAGAAAGCGTCTAGCCATGGCGTTA 246
                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                       1 GCAGAAAGCGTCTAGCCATGGCGTTA 26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAAAGCGTCTAGCCATGGCGTTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
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TELEFAX: (415) 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CARROLL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 281 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE: MEDLEN & CARROLL
                                                                                             Application US/09940925A
o. US20030054338A1
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o. US20030054338A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                        .inear
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                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO: 129:
                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                          Score 26; DB 9;
Pred. No. 0.0027;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US2003
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 131: SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/941,193A
FILING DATE: 28-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET,
                                                                                                                                                                                                                                                                                                                                                              OLIVE, DAVID M. TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 GCAGAAAGCGTCTAGCCATGGCGTTA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                 ZIP: 94104
                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                        STATE: CALIFORNIA
                                                                                                                                                                                                                                           CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415)
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/940,925A FILING DATE: 10-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 281 base pairs
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Pred. No.
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0.0027;
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RESULT 15
US-09-941-193A-125
; Sequence 125 App
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-09-941-193A 123
                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-941-193A; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match Best Local Similarity Matches 26 Conserv
                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 26; Conservative 0;
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INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE,DOCKET NUMBER: FORS-01756
REFERENCE,DOCKET NUMBER: FORS-01756
RELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
FORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: |
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GCAGAAAGCGTCTAGCCATGGCGTTA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/941,193A FILING DATE: 28-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                    STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 281 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09941193A
o. US20030108873A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHOGENS.
                                      Score 26; DB'9; Length 281; Pred. No. 0.0027; Mismatches 0; Indels
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11 GCAGAAAGCGTCTAGCCATGGCGTTA 36

Search completed: July 11, 2003, 15:01:56 Job time: 71.164 secs

sp72a05.y saf46h05. saq55d09. 602439575

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Result
No.
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Maximum Match 1008
Listing first 45 s
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Maximum DB seq
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                                                                                                                  Score
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                                                                                                                                                                                                                              AUTHORS
                                                            Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                     Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 549)

""" Long Pambo T Cimmons I Henry
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 Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 542.
Location/Qualifiers
                                                                                                                                                                          Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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A1255537 u155904 y
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BM168779 EST571102
BE6322435 uv56c06. y
BG146531 mab93b06.
BJ184088 BJ18408
BB6522435 uv56c06. y
BG146531 mab93b07
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                   GCAGAAAGCGTCTAGCCATĞGCGTT 25
                                                                                                                                                                                                                                                                                                     Email: rwing@clemson!edu
                                                                                                                                                                                                                                                                                                                                                                                                            Wing,R.A., Frisch,D., Yu,Y., Main,D., Ra
D., Wood,T.C., Leslie,A. and Wilkins,T.
An integrated analysis of the genetics,
of the cotton fiber
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Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; copre eu
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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lemson University 00 Jordan Hall, Clemson, SC 29634, U
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                                                                                                                                                              tissue_type="Fibers isolated from
                                                                                                                                                                         clone_lib="Gossypium arboreum"
                                                                                                                                                                                                    /db_xref="taxon:29729"
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/strain="AKA" .
                                                                                                                                                                                              'CLone="GA
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   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, develop
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                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
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Seq primer: TANTACGACTCACTATAGGG
High quality sequence stop: 407.
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                                                                                                                                                                                                                                                                                                                                                                                                                             170
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                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:29729"
/clone="GA_Ea0015c07r"
/clone_lib="Gossypium arboreum 7-10
/tissue_type="Fibers isolated from
dpa"
                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1:
130 c 139 g 171 t
                                                                                                                                                        GI:21091981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cultivar="8400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Gossypium arboreum"
/strain="AKA"
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                                                                                                                                                                                                                                                                                                                                                                 88.0%;
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clone GA__Ea0015G07r, mRNA
                                                                 II; Malvales;
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                                                                                                                                                                                                                                                                                                                                              Score 20.2; [Pred. No. 99; 0; Mismatches
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arboreum 7-10 dpa fiber library Gossypium
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                                                              Malvaceae;
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development,
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From bolls harvested 7-10
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                                                           Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                       610;
                                                                         eudicots;
 and evolution
                                                                                                                                                                                                       EST 22-MAY-2002
                                                                                      Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 09-JAN-2002
                                                                                                                                                                                       Gossypium
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RESULT 5
BQ401354
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                        Gossypium arboreum.
Gossypium arboreum.
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; sudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                     Email: rwing@clemson.edu
Total High Quality bases = 584
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                     100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                              Wing.R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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BQ401354
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Seg primer: TAATACGACTCACATATAGGG
High quality sequence start: 6
High quality sequence stop: 632.
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100 Jordan Hall, Clemson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ401354.1 GI:21089041
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Fax: 864 656 4293
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                                                                                                                                                                                                                                                               Unpublished (2000)
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The Hall, Clemson,
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__Ed0001A07f Gossypium arboreum 7-10 dpa fiber library
Doreum cDNA clone GA__Ed0001A07f, mRNA sequence.
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                                                                                                                                                                                                                                                  tact: Wing RA
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                                                                                                          quality sequence stop:
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                                             /organism="Gossypium arboreum"
/strain="AKA"
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/clone_lib="Gossypium arboreum
/tlssue_type="Fibers isolated f
 /db_xref="taxon:29729"
/clone="GA__Ed0001A07f"
                                /cultivar="8400"
                                                                                          ocation/Qualifiers
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strain="AKA"
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-Pred. No. 1e+02;
0; Mismatches 3;
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RESULT 7
BG440823
LOCUS
DEFINITION
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KEYWORDS
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Query Match
Best Local :
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31
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                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Seq primer: Teauence stop: 642.
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100 Jordan Hall, Clemson, SC 29634, U.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                1 GCAGAAAGCGTCTAGCCATGGCGTT 25
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BG441998
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing, R.A., Frisch, D
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Location/Qualifiers
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                                                                                                                                               /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
    128 c    146 g    181 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                        tissue_type="Fibers isolated
                                                                                                                                                                                                                                        /db_xref="taxon:29729"
/clone="GA__Ea0015G07f"
/clone_lib="Gossypium arboreum 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'lab_host="E. coli"
                                                                                                                                                                                                                                                                                                               strain="AKA"
                                                                                                                                                                                                                                                                                                                            organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                             cultivar-"8400"
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88.0%;
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Pred.
                                                                                 Score 20.2; DB Pred. No. 1e+02;
                                                                   Mismatches
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No. 1e+02;
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harvested 7-10
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.BG440823 GA\_\_Ea0010F07f Gossypium arboreum

mRNA 7-10 dpa

fiber library

EST 15-MAR-2001

Gossypium

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REFERENCE
AUTHORS
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BE055545
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                                                                                                                                                                                                 Gossypium arboreum

Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                      GAL_Ea0004L16f Gossypium arboreum cDNA clone GA__F BE055545
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          lemson University Genomics Institute
Lemson University
00 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGAAAGCCTCTAGCCATGACTTT 42
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                                                                                                                             ng,R.A., Frisch,D., Yu,Y., Main,D., Ra
, Wood,T.C., Leslie,A. and Wilkins,T.
integrated analysis of the genetics,
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integrated analysis of the genetics, development, and evolution
the cotton fiber
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                                                                            Jun 8,
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                                                            tact: Wing RA
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:29729"
/clone="GA_Ea0010F07f"
/clone_lib="Gossypium arboreum
/tlssue_type="ribers isolated f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cultivar="8400"
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                                                                                                                 fiber
                                                                              this sequence version replaced
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                                                                                                                                                               Yu,Y., Main,D.,
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e,A. and Wilkins,T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.2; DB 12
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                      779 bp mRNA
m arboreum 7-10 dj
_Ea0004L16f, mRNA
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s harvested 7-10
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                                                                                                                                                                                                   High quality sequence start: 4
High quality sequence stop: 535
Location/Qualifiers
                                                                                                                                                                                                                                                                             100 Jordan Hall, Tel: 864 656 7288 Fax: 864 656 4293
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Eukaryota; Viridiplantae;
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BF278075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax:
                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF278075.1 GI:11209061
                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                            emson University
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
                                                                        /db_xref="taxon:29729"
/clone="GA_Eb0038A09f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tlssue_type="Fibers isolated from bolls harvested 7-10"
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              /note="Vector: pBK-CMV; Site_1: 194 c 148 g 298 t
                                                                                                                                         cultivar="8400"
                                                                                                                                                         strain="AKA"
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                                              lab_host="E. coli"
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mm arboreum 7-10 dpa fiber library Gossypium
_Eb0038A09f, mRNA sequence.
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7 others
                 EcoRI; Site_2: XhoI"
2 others
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Score 20.2;

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Length 840;

A linear EST: dpa fiber library

EST 22-MAY-2002

Gossypium

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Conton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K., Lazo,G.R., Rausch,C.J., Wilson,C. and Woo,J.

The structure and function of the expressed portion of the genomes - Chinese Spring whole plant cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aestivum cDNA clone WHE
BQ839191
BQ839191.1 GI:22143513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: oandersn@pw.usda.gov
Sequences have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 5105595818
                                                                                                   Similarity
                          GCAGAAAGCGTCTAGCCATGGCGTT 25
        GCAGAAGGCGTGGCGCCATGGCGTT
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Buchanan Street, Albany, CA 94710, USA
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                                                                                                                                                                                                                                   greenhouse were collected at University of California, Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total RNA was prepared from leaves (young leaf and third leaf), whole roots, crown, steam and sheath tissues, and then equal quantities of RNA were pooled from the these samples. PolyA was purified from the pooled RNA, a cDNA library was made, and the cDNA closes were in vivo excised to give pBluescript SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak) at the University of California, Davis. Colony plating, plasmid DNA preparations and DNA
                                                                                                                                                                              sequencing were performed in the OD other authors)."
183 c 231 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plant
tissues from wheat cv. CS grown to full tillering stage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
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lone_lib="Wheat CS whole plant cDNA library"
                                                                                                   71.5%;
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Pred. No. 5.
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GA__Ed001
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                                                                                                                                                                                                                                                                                                                                                                                                                1 GCAGAAAGCGTCTAGCCATGGCGTT 25
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 313)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simp
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J.
                                                                                                                                                                                                                                       RC4-NN0055-060400-011-f09
AW896937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Total High Quality bases = 442
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                     AW896937.1
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Fax: 864 656 4293
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poreum cDNA clone GA__Ed0087E10f, mRNA sequence.
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/clone="GA_Ed0087E10f"
/clone_11b="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AKA"
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DB 14;

Length

688;

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Gaps

mRNA

linear

sapiens cDNA,

mRNA sequence EST 24-MAY-2000

Costa, F.F.,

Simpson, D.H.,

O'Hare

Euteleostomi;

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JOURNAL
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AUTHORS
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Eukaryota; Viridiplantae;
                                                                                                                                                                               Contact: Schulman AH
Institute of Biotechnology
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                                                                                                                                                                                                                         Unpublished (2002)
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                                                                                                                                             versity of Helsinki
O.Box 56 (Viikinkaari 6A);
                                                                                                                                                                                                                                                                                                                ermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tp://www.ludwig.org.br/scripts/gethtml2.
-011-f09&t3=2000-04-06&t4=1)
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcript
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Site_2: Smal; A mini-library was made by cloning products
                                                          /cultivar="Saana"
                                                                         /organism="Hordeum vulgare"
                                                                                                             Location/Qualifiers
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/clone_lib=
                                     /db_xref="taxon:4513"
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                    clone="S0000200049A08F1"
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/ta; Liliopsida; Poales; Poaceae; Pooidea
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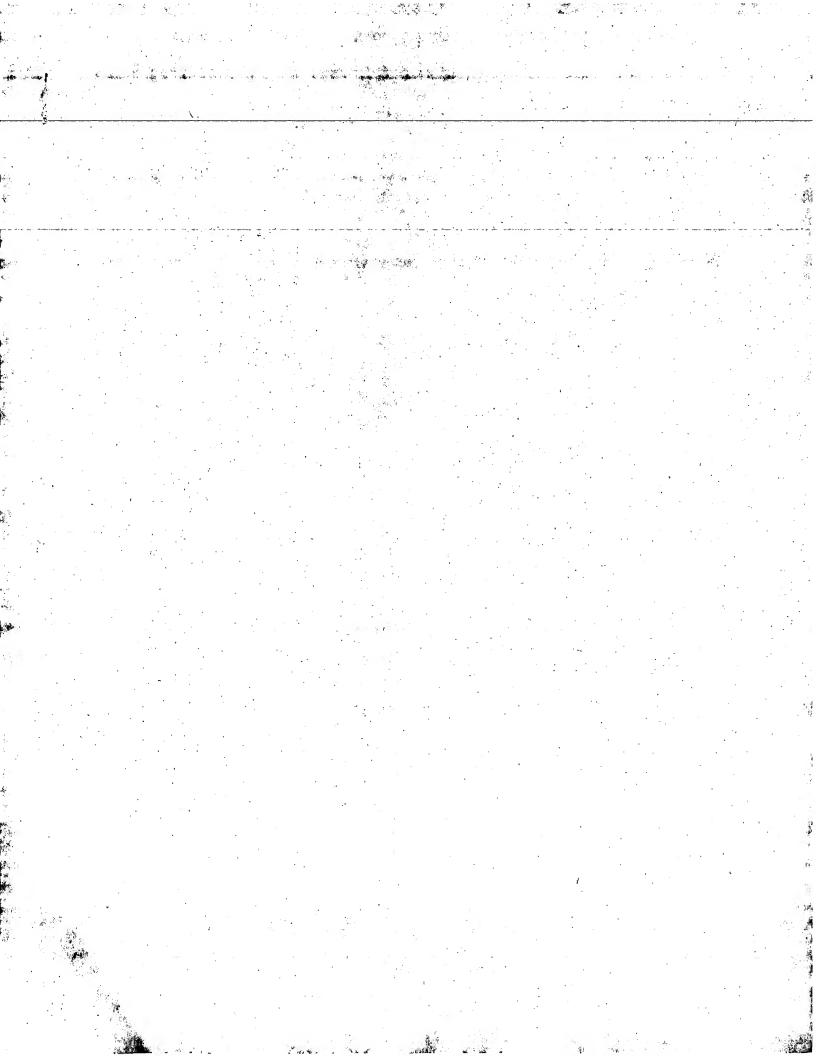
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Plate: 205 row: O column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pieter (pieter@dejong.med.buffalo.edu). Clones may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the mouse BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mail: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 Medical Center Dr.,
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                                                                                        selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). **
175 c 159 g 202 t
                                                                                                                                                           'note-"Organ: Kidney/Brain; Vector: pBACe3 6: Site_1:
ECORI; Site_2: ECORI; Pemale C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="RPCI-23-205015"
                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                               'lab_host="DH10B"
                                                                                                                                                                                                                                                   'sex="Female"
                                                                                                                                                                                                                                                                      clone_lib="RPCI-23"
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/note="1 day after pollination"
59 c 57 g 61 t
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                    70.0%;
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Rodentia;
Score 18.2; DB 17;
Pred. No. 9.4e+02;
0; Mismatches 3;
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Pred. No. 4
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Sciurognathi;
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                                    DB 17;
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thi; Muridae; Murinae; Mus
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1 GCAGAAAGCGTCTAGCCATGGCG 23

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701 GCAGAAAGTGTCTAGTCAAGGCG 723

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AUTHORS
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Best Local Similarity
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                                                                                             322 GCAGAAAGAGTCAACCCATGTAGTTA 297
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                                                                                                                        1 GCAGAAAGCGTCTAGCCATGGCGTTA 26
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Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pax: +55-11-2707001
mail: asimpson@ludwig.org.br
mail: sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
[http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL2&t2=IL2-UT0073-
[21100-232-D04&t3-200-11-12&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ntact: Simpson A.J.G.
boratory of Cancer Genetics
idwig Institute for Cancer Research
ia Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                   /note-"Organ: uterus_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'dev_stage="Adult"
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Pred. No. 7
                                                                                                                                                                                           Mismatches
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7.7e+02;
hes 5; Indels .
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                         'SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:
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/NA2001B.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Partial sequence o	AAV70455	19	239	100.0	28	9	Q
Hepatitis C virus	ABL46070	24	232	100.0	28	8	o
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Hepatitis C virus	AAQ63223	14	57	100.0	28	4	ი
Reverse PCR primer	AAH25414	22	28	100.0	28	w	
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Hepatitis C virus	AAT67194	18	. 28	100.0	28	1	
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## ALIGNMENTS

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AIT AAT67194 standard; DNA; 28 BP.

13-FEB-1998 (first entry)

AAT67194;

Hepatitis C virus (HCV) RNA amplification primer ST778AA.

Hepatitis C virus; HCV; ST778AA; reverse transcription PCR; RT-PCR; detection; PCR primer; ss.

Synthetic.

EP776981-A2

04-JUN-1997.

21-NOV-1996;

96EP-0118704

29-NOV-1995; 9508-0007739

(HOFF ) HOFFMANN LA ROCHE & CO ĄG

Tsang SY;

WPI; 1997-291296/27.

Oligonucleotide primers for hepatitis C virus  ${\tt RNA}$  amplification by polymerase chain reaction

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RESULT 2
AAV59059
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Best Local
                             S1 is a sequence of
nucleotides; and Nu
having an exocyclic
                                                   This sequence represents a primer for a fragment of HCV, and is an example of an oligonucleotide of the invention. The oligonucleotides of the invention are of the formula 5'-S1-Nu-3' or 5'-S1-Nu-S2-3', where
                 1-10C alkyl, alkoxy,
                                                                                                         Example
                                                                                                                                         Oligo-nucleotide(s)
                                                                                                                                                              WPI; 1998-482929/42
                                                                                                                                                                                     Will SG,
                                                                                                                                                                                                         (HOFF )
                                                                                                                                                                                                                               20-MAR-1997;
                                                                                                                                                                                                                                                  12-MAR-1998;
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                                                                                                                                                                                                                                                                                               EP866071 - A2
                                                                                                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                                                                  modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV59059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV5905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to amplify a 250 base pair product from the HCV genome. This can be used to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sensitivity. Amplification of HCV nucleic acid using this 100 times more efficient than amplification with prior art
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        downstream primer ST778AA is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                cytomegalovirus.
                                                                                                        6; Page 16;
                                                                                                                                                                                                      HOFFMANN LA ROCHE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŠT778AA
                                                                                                                             for nucleic
                           exocyclic amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                   Young KKY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV; nucleic acid
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                            97US-0041127
                                                                                                                                                                                                                                                 98EP-0104461
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28
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                      38pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                            containing N-substituted acid amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HCV)
             amino group substituted optionally substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 10 C; 5 G; 3 T; 0
on incleotides; S2 is a sequence or 150 nucleotides; S2 is a sequence or pyrimidine base a nucleotide with a purine or pyrimidine base ino group substituted by CHRIR2; R1, R2 are H, ray and ly substituted phenyl, phenoxy or option
                                                                                                                                                                                                                                                                                                                "optionally benzylated, methylated,
    nitrobenzylated"
                                                                                                                                                                                                                                                                                                                                                         "optionally benzylated"
                                                                                                                                                                                                                                                                                                                                                                                                      .
2
                                                                                                                                                                                                                                                                                                                                                                                         "optionally benzylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA by reverse
                                                                                                     English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amplification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription PCR.
n the 5' untranslat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the amplification or
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                                                                                                                                    useful as
                                                                                                                                                                                                                                                                                                                        or
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           optionally
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Query Match
Best Local Similarity
Matches 28; Conser

Conservative

0;

Mismatches

0,

Gaps

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100.0%;

Score 28; Pred. No.

0.0028 DΒ

Length Indels

GCAAGCACCCTATCAGGCAGTACCACAA

Sequence

28

BP; 10

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10 C;

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3 T; 0 other;

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                         The specification describes a composition of magnetic glass particle which contain at least one magnetic object with a mean diameter between 5-500 nm. The composition is useful for the purification of nucleic acids. The composition can be used to process large quantities of nucleic acid samples, because it does not involve the particles being the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the compos
                                               nucleic acid samples, because it does not involve the particles of centrifuged or the fluids being drawn through glass fiber filters PCR primers AAHS4413-14 were used to amplify HCV DNA fragments. The amplified fragment can be purified using the method of the invention
                                                                                                                                                                                                                                                                                                                            or RNA
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-381247/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weindel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-1999;
12-MAY-2000;
                                                                                                                                                                                                                                                                         Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOFF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reverse PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH25414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH25414 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substituted naphthyl. The oligonucleotides are useful as primers for nucleic acid amplification, preferably by polymerase chain reaction. of the modified primers reduces non-specific amplification, especial primer dimer formation, with a concomitant increase in the yield of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28 BP; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intended
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                                                                                                                                                                                                                                                                                                                         composition of magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCAAGCACCCTATCAGGCAGTACCACAA 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glass particle; nucleic acid purification; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          target.
                                                                                                                                                                                                                                                                         Page 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Riedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99EP-0122853.
2000EP-0110165.
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                                            can be purified
                                                                                                                                                                                                                                                                  105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used
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derivatisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Geiger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplify a HCV DNA
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                                                                                                                                                                                                                                                                                                                                              glass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DE Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 T; 0
                                                                                                                                                                                                                                                                                                                                              particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with a p-(t-butyl)benzyl-residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amplification, especially ncrease in the yield of the
                                                                                                                                                                                                                                                                                                                                           purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                          of.
                                                                                                                                                                                     glass particles,
diameter between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                           being
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                                                                                                                                                                                                                                                                                                                                         DNA
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GCAAGCACCCTATCAGGCAGTACCACAA 28

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RESULT 5
AAT11272
ID AAT1
XX
AC AAT3
DT 26-,
XX
DE Hep
XX
DE Hep
XX
DE Hep
XX
OS Heg
XW
OS Heg
XX
PD
XX
PD
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
AAQ63223/c
ID AAQ63223 standard; R
XX
AC AAQ63223;
XX
XX
XX
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Best Local S
Matches 28
                                                                              Antisense; therapy; hepatitis C virus; clone 2-1; ss. (
                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that of the target region of probes (AAQ53257-Q53260) used in the detection of hepatitis C virus (HCV) using a 11:2 probe design. It corresponds to positions 246-302 of the 5' UTR of the
                              JP07303485-A
                                                      Hepatitis C virus
                                                                                                                                    Hepatitis C virus partial 5'-UTR antisense RNA AS15
                                                                                                                                                              26-JUN-1996
                                                                                                                                                                                          AAT11272;
                                                                                                                                                                                                                    AAT11272 standard;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57 BP; 9 A; 9 C; 23 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 26; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amplifying known RNA target for use in diagnosis of HIV and HCV infection - by treating sample RNA with oligo-nucleotide probe, extending probe by reverse transcription of target, dissociating probe from target, hybridising 2nd probe with 1st, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-405844/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carrino JJ, Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection; HCV; 11:2 probe design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus probe target region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9205-0891543
                                                                                           ; complementary; HCV; 5'-untranslated region;
inhibition; infection; treatment; stem-loop;
                                                                                                                                                                                                                  RNA; 186 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŖĮ,
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RESULT 6
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                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                   cellular organism;
                                                                                                                                                                                                                                                                                                                                                           DNA comprising consensus endodogmatic sequence/exodogmatic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus (HCV) anti:sense RNA - inhibits HCV structural gene expression in vivo for treatment of HCV infection
                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                             ABL41919
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL41919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 186 BP; 41 A; 65 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2-1. The 5'-UTR includes several stem-loop sequences. The antisense RA-1 is useful for inhibiting expression of HCV structural genes and thereby inhibiting viral replication in vivo. The antisense therapy can be used in addition to conventional interferon treatment of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a specifically claimed example of RNA that is complementary (i.e. antisense) to part of the 5' untranslated region of the hepatitis C virus genome sequence contained in clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 10; 12pp; Japanese
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                                                                                                                                                                                                                                                                           stem_loop
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92..104
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10..14
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                                                                                                                                                                                                                                                                                                                                    pathogen; retroviral particle; probe; ss
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3; Mismatches
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microbes and/or determination of genotype, as primers for polymerase chain reaction amplification and therapeutically for blocking replication of pathogens, e.g. as ribozymes. Particularly, the probes
                                                                                                      agents without prior DNA or RNA extraction. The probes enable detection of nucleic acids in sections of living or immobilised, frozen or fixed tissues. Probes of the invention are useful for detecting viral (including oncogenic), bacterial, animal and plant nucleic acid.
                                                                                                                                                             non-contagious molecular probes which are used for detecting nucleic acids. The process that takes account of the forms of presentation of cellular organisms during the life cycle, or where these forms depend on different chemical, biological and physical states of the organism. The process is a contamination free diagnostic method for direct quantitative and qualitative analysis and gene typing of infectious
                                                                                                                                                                                                                                                         The specification describes a process
                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 25pp; French.
                                                                                                                                                                                                                                                                                                                                formulating molecular probes,
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                                                                                                                                                                                                                                                                                                                                                                                                                          (MENO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171...173
                        retroviral particles circulating in body fluids or the present sequence represents a sequence comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .93..195
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                                                                                                                                                                                                                                                                                                                 presentation
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            exodogmatic sequence
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                                                                                                                                                                                                                                                                                                             in organisms
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Best Local

Similarity

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DB 24; 0.0038;

Sequence 232 BP; 40

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Sequence

209

BP; 48

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59

64 G;

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                                 I probe complementary to at least a portion of the folded target; and CC probe /folded target and probes so that the probe hybridises to form a CC probe /folded target complex. Also provided are methods for determination CC nucleic acids targets; and for analysis of nucleic acid structure formation in nucleic acid targets; for analysing folded CC methods can be used for the detection and characterisation of nucleic acid structures. The CC acid sequences to detect the presence of pathogenic nucleic acid complex associated with disease and cancers, and the CC identification of the source of nucleic acids found in forensic samples, CC analysis of both strands (e.g. the sense and antisense strands) and are qualitative, quantitative and positional analysis. The methods are powerful in that they allow for analysis of longer analysis of nucleic acid than current methods of analysis of longer CC analysis of nucleic acid than current methods are solid support). The methods are powerful in that they allow for analysis of longer analysis of nucleic acid than current methodologies. Sequences of the methods and cancers and for high-level made and positions of analysis of longer analysis of nucleic acid than current methodologies. Sequences of comparatitis C virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TT XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to methods and compositions of detection and characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (a) providing: (i) stranded region and at least 1 single stranded region; and (ii) at least 1 single stranded region; and (ii) at least 1 single stranded region; and (iii) at least 1 single stranded region; and (iv) at least 1 single stranded region; at least 1 single stranded region; at least 1 single stranded region; at least 1 single stranded region; at least 1 single stranded region; at least 1 single stranded region stranded region stranded region stranded region stranded region stran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection and characterisation of nucleic acid sequences - by a folded target and one or more probes to form a probe/folded complex and detecting and characterising the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 172-173;
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Lyamichev
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05-MAY-1997;
19-SEP-1997;
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Neri BP,
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97US-0851588.
97US-0934097.
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                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid characterisation; hybridisation; cer; forensic; paternity; multiplexing; HCV; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dahlberg JE
Prudent JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
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                  HCV
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target
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Query Match

Local

Similarity

100.0%;

Score 28; DB 19; Pred. No. 0.0039;

DB 19;

Length 232;

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ABL46070/c
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                                                                               Query Match
Best Local (
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                              that form an extension product are identified as the oligonucleotides which can interact with the folded target nucleic acid. Oligonucleotides from the present invention can be used in novel detection methods for clinical diagnostic purposes, including the detection and identification of pathogenic organisms (e.g. HIV). The method allows the ability to rapidly analyse nucleic acid structures. ABI46034 to ABI46367 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                            The present invention describes a method for identifying oligonucleotides with desired hybridisation properties to nucleic acid targets containing secondary structure. The method comprises amplifying a target nucleic acid having at least one accessible and one inaccessible site. Primers
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 366; 409pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 product under
                                                                                                                                                                                                                                                                                                                                                                                                           Identifying oligonucleotides hybridizing to nucleic acids containing secondary structure, useful in clinical diagnosis, comprises identifying primers that interact with the target to form an extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-049698/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lyamichev .V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2000; 2000US-212308P
15-JUN-2001; 2001US-0212308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C. virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid accessible hybridisation site; detection; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL46070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL46070 standard; DNA; .232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2001; 2001WO-US19401
 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
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                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAGCACCCTATCAGGCAGTACCACAA 205
GCAAGCACCCTATCAGGCAGTACCACAA 205
                              GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                             232 BP;
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 amplification conditions
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                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification; nucleic acid structure;
                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ħ
                                                                                                                               65 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dong F, Neri BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿₽.
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                                                                                                                               76 G;
                                                                             Score 28; DB 24
Pred. No: 0.0039
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                             51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #86 SEQ ID NO:37.
                                                                                              DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vener IT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                           Length 232;
                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                             an extension
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                                                            Gaps
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RESULT 9
AAV70455/c

Query Match Best Local S Matches 28

Similarity

100.0%; 100.0%;

Score 28; DB 19; Pred. No. 0.0039;

DB 19;

Length 239; Indels

Conservative

0;

Mismatches

0,

0

Gaps

9

239 GCAAGCACCCTATCAGGCAGTACCACAA 212

GCAAGCACCCTATCAGGCAGTACCACAA 28

Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 other;

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Anderson TA, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I probe complementary to at least a portion of the folded target; and (b) mixing the target and probes so that the probe hybridises to form a probe /folded target complex. Also provided are methods for determination of structure formation in nucleic acid targets; for analysing folded nucleic acids targets; and for analysis of nucleic acid structures. The methods can be used for the detection and characterisation of nucleic acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles of mammalian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous associated with constants of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous associated with constants of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous as well as in paternity determinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods and compositions of detection and characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (a) providing: (i) a folded target having a DNA sequence comprising at least 1 double folded tegion and at least 1 single stranded region; and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (ii) at least stranded region and (iii) at least stranded region at least stranded region and (iii) at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded region at least stranded reg
                                                           ideal for high-level multiplexing. The products produced are amenable to qualitative, quantitative and positional analysis. The methods may be performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer fragments of nucleic acid than current methodologies. Sequences AAV/0453-61 represent partial sequences of different amplicons of hepatitis C virus (HCV) subtypes la, lb, 2c and 3a. These partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection and characterisation of nucleic acid sequences - by mixing a folded target and one or more probes to form a probe/folded target complex and detecting and characterising the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-610317/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV70455 standard; DNA; 239 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis of both strands (e.g. the sense and antisense strands) and are
      are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
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Neri BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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97US-0851588
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(HCV) subtypes 1a, 1b, 2c and 3a. for identifying the HCV subtypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; forensic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prudent JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahlberg JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŗ
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RESULT 10 AAV70459/c

AAV70459

standard; DNA;

239

ВP

Partial

sequence of

HCV subtype

10

amplicon

08-APR-1999 AAV70459

(first

entry)

Nucleic

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밁
                             Š
                                                                          Query Match
Best Local (
                                                             Matches
                                                                                                                                                                                           acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles of mammallian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous analysis of both strands (e.g. the sense and antisense strands) and are ideal for high-level multiplexing. The products produced are amenable to qualitative, quantitative and positional analysis. The methods may be performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer fragments of nucleic acid than current methodologies. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1998;
05-MAY-1997;
19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection a folded t
                                                                                                                        Sequence
                                                                                                                                               AAV70453-61 represent partial sequences of different amplicons hepatitis C virus (HCV) subtypes 1a, 1b, 2c and 3a: These part: sequences are used for identifying the HCV subtypes.
                                                                                                                                                                                                                                                                                                                                                                                       of structure formation in nucleic acid targets; for analysing folded nucleic acid structures. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9850403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis,
                                                                                                                                                                                                                                                                                                                                                                       methods can be used for the detection and characterisation of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                    probe /folded target complex. Also provided are methods for determination
                                                                                                                                                                                                                                                                                                                                                                                                                                   folded target having a DNA sequence comprising at least 1 double stranded region; and (11) at least 1 probe complementary to at least a portion of the folded target; and (b) mixing the target and probes so that the probe hybridises to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  character|isation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to methods and compositions of detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-610317/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (THIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection;
 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of detection and characterisation comprises: (a) providing: target having a DNA sequence comprising at least 1 double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid detection; nucleic acid characterisation; hybridisation; on; disease; cancer; forensic; paternity; multiplexing; HCV; d
                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA,
GCAAGCACCCTATCAGGCAGTACCACAA
                           GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         target and or
and detecting
                                                                                                                        239 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and characterisation of nucleic acid sequences - by target and one or more probes to form a probe/folded nd detecting and characterising the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 172;
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brow MAD,
Neri BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0851588
97US-0934097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0034205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US03194
                                                                                                                       45 A; 64 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic
                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dahlberg JE,
Prudent JR;
                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                     77 G; 53 T; 0 other;
                                                                          Score 28; DB
Pred. No. 0.00
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences
 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dong
                                                                        0.0039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region; and (ii) at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence changes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fors
                                                                                       Length
                                                      Indels
                                                                                                                                                               licons of partial
                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mixing
target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                one
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RESULT 12
ABL46069/c
ID ABL460
XX
AC ABL460
XX

standard;

DNA;

239

₽P

ABL46069 ABL46069

Hepatitis C 26-APR-2002

virus partial sequence #85

Đ

NO:36

(first entry)

ğ

239 GCAAGCACCCTATCAGGCAGTACCACAA 212

GCAAGCACCCTATCAGGCAGTACCACAA 28

Query Match Best Local Matches

28; Similarity

Conservative

0;

Mismatches

0

Indels

0

Gaps

0,

100.0%; 100.0%;

Score 28; DB 24 Pred. No. 0.0039

DB 24;

Length 239

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PART OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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XX
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                                                                                                that form an extension product are identified as the oligonucleotides which can interact with the folded target nucleic acid. Oligonucleotides from the present invention can be used in novel detection methods for clinical diagnostic purposes, including the detection and identification of pathogenic organisms (e.g. HIV). The method allows the ability to rapidly analyse nucleic acid structures, ABI46034 to ABI46367 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying oligonucleotides hybridizing to nucleic acids containing secondary structure, useful in clinical diagnosis, comprises identifying primers that interact with the target to form an extensipproduct under amplification conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2000;
15-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL46065;
Sequence 239 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 365; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-049698/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid accessible hybridisation site; detection; hybridisation; characterisation; identification; nucleic acid structure; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL46065 standard; DNA;
                                                                                                                                                                                                                                                                                                                                secondary structure. The method comprises amplifying a target nucleic acid having at least one accessible and one inaccessible site. Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200198537-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus partial sequence #72 SEQ ID NO:32
                                                                                                                                                                                                                                                                                                                                                                                                          desired hybridisation properties to nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-212308P.
2001US-0212308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US19401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry
                                                                         'n
45 A; 63 C;
                                                                 ic acid structures. exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dong F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
78 G; 53 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neri BP,
                                                                 es. ABL46034 to of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the target to form an extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vener
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H
                                                                                                                                                                                                                                                                                                                                                                                                             targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonucleotides
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AAV70457/c
ID AAV70
XX AAV70
XX AAV70
XX AAV70
XX O8-AP
DT 08-AP
XX Nucle
KW Infec
XX Hepat
XX Hepat
XX Hoose
XX Hoose
XX 12-NC
XX 05-MA
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                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secondary structure. The method comprises amplifying a target nucleic acid having at least one accessible and one inaccessible site. Primers that form an extension product are identified as the oligonucleotides which can interact with the folded target nucleic acid. Oligonucleotides from the present invention can be used in novel detection methods for clinical diagnostic purposes, including the detection and identification of pathogenic organisms (e.g. HTV). The method allows the ability to rapidly analyse nucleic acid structures. ABI46034 to ABI46367 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                 AAV70457 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying oligonucleotides hybridizing to nucleic acids containing secondary structure, useful in clinical diagnosis, comprises identifying primers that interact with the target to form an extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyamichev V, Allawi H,
05-MAY-1998;
                                                      WO9850403-A1
                                                                                                                  Nucleic acid detection; nucleic acid characterisation; infection; disease; cancer; forensic; paternity; multip
                                                                                                                                                           Partial sequence of HCV subtype 2b amplicon #74.
                                                                                                                                                                                           08-APR-1999
                                                                                                                                                                                                                        AAV70457
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 239 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for identifying oligonucleotides with desired hybridisation properties to nucleic acid targets containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 366; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-2000; 2000US-212308P.
15-JUN-2001; 2001US-0212308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2001; 2001WO-US19401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200198537-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid accessible hybridisation site;
                            12-NOV-1998
                                                                                     Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product under amplification conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-049698/06
                                                                                                                                                                                                                                                                                                                             239
                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                        (first entry)
98WO-US03194.
                                                                                                                                                                                                                                                                                                                                                                                                                                            45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification; nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 64 C;
                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dong F, Neri BP, Vener
                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                               forensic; paternity;
                                                                                                                                                                                                                                                                                                                                                                                                                                           77 G;
                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 24;
Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC.
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            53 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection; hybridisation;
cid structure; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                multiplexing;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 239;
                                                                                                                              hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                  HCV;
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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AAV70456/c ID AAV704

standard;

DNA;

240

RESULT 14

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240

213

0;

Nucleic acid detection; nucleic acid characterisation; hybridisation; infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds

Partial sequence of HCV subtype la amplicon #73

08-APR-1999

(first entry)

AAV70456; AAV70456

12-NOV-1998

WO9850403-A1 Hepatitis C virus

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                                     Query Match
Best Local S
Matches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1998;
05-MAY-1997;
19-SEP-1997;
                                                                                                                                          of mammalian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous analysis of both strands (e.g. the sense and antisense strands) and are ideal for high-level multiplexing. The products produced are amenable to qualitative, quantitative and positional analysis. The methods may be performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer fragments of nucleic acid than current methodologies. Sequences ANY0453-61 represent partial sequences of different amplicons of hepatitis C virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used for identifying the HCV subtypes.
                                                                                                                                                                                                                                                                                                                                                                        method of detection and characterisation comprises: (a) providing: (1) a folded target having a DNA sequence comprising at least 1 double stranded region and at least 1 single stranded region; and (1) at least 1 probe complementary to at least a portion of the folded target; and (b) mixing the target and probes so that the probe hybridises to form a probe /folded target complex. Also provided are methods for determination of structure formation in nucleic acid targets; for analysing folded nucleic acids targets; and for analysis of nucleic acid structures. The methods can be used for the detection and characterisation of nucleic acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection and characterisation of nucleic acid sequences - by a folded target and one or more probes to form a probe/folded complex and detecting and characterising the complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-610317/51.
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                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterisation
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 1 GCAAGCACCCTATCAGGCAGTACCACAA 28
                                       28;
                                                         Similarity
                                                                                                                  240
                                       Conservative
                                                                                                              BP; 47
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97US-0851588.
97US-0934097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                              A; 64 C;
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                                     Score 28; DE Pred. No. 0.(0; Mismatches
                                                                                                              74 G;
                                                                                                                55 T; 0 other;
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                                                       0.0039
                                                                            DB 19;
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Best Local :
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WO9850403
                                       Hepatitis C virus
                                                                                                     Nucleic
                                                                                                                                               Partial
                                                                                                                                                                                        08-APR-1999
                                                                                                                                                                                                                                AAV70458
                                                                                                                                                                                                                                                                     AAV70458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of mammalian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous analysis of both strands (e.g. the sense and antisense strands) and are ideal for high-level multiplexing. The products produced are amenable to performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to methods and compositions of detection and characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (a) providing: (1) a folded target having a DNA sequence comprising at least 1 double stranded region and at least 1 single stranded region; and (ii) at least 1 probe complementary to at least a portion of the folded target; and (ii) at least 1 probe complementary to at least so that the probe hybridises to form a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragments of nucleic acid than current methodologies. Sequences AAV70453 61 represent partial sequences of different amplicons of hepatitis C virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used for identifying the HCV subtypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-1998;
05-MAY-1997;
19-SEP-1997;
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                                                                  acid detection; nucleic acid characterisation; hybridison; disease; cancer; forensic; paternity; multiplexing;
                                                                                                                                    sequence of HCV subtype 3a amplicon #81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Prudent JR;
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Pred. No. 0.0039;
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of structure formation in nucleic acid targets; for analysing folded nucleic acids targets; and for analysis of nucleic acid structures. The methods can be used for the detection and characterisation of nucleic acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or allele of mammalian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous
                        qualitative, quantitative and positional analysis. The methods may be performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer fragments of nucleic acid than current methodologies. Sequences AAV70453-61 represent partial sequences of different amplicons of hepatitis C virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used for identifying the HCV subtypes.
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05-MAY-1997;
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                                                                                                                                                                   analysis of both strands (e.g. the sense and antisense strands) and are ideal for high level multiplexing. The products produced are amenable to
                                                                                                                                                                                                                                                                                                                                                                              probe /folded_target complex. Also provided are methods for determination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to methods and compositions of detection and
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Lyamichev VI,
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One (i) a

Sequence 240 BP; 45 A; 66 C; 79'G; 50 T; 0 other;

밁 Query Match Best Local Matches Local 240 1 GCAAGCACCCTATCAGGCAGTACCACAA 28 l Similarity 28; Conserv GCAAGCACCCTATCAGGCAGTACCACAA 213 Conservative 100.0%; 0; Score 28; Pred. No. Mismatches 0.0039; DB 19; 0; Length 240; 0; Gaps

Search completed: July 10, 2003, 19:52:42 Job time: 60.0831 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Database
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Maximum Match 100%
Listing first 45 summaries
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ch 1 Si 28;	T 1 1738-928-2 1738-928-2 NERAL INFORMATION APPLICANT: TSANG, TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TOWNESSEE: HOSE STREET: 340 Kil CITY: NULLEY STATE: NJ COUNTRY: ULLEY STATE: NJ COUNTRY: U.S.A. ZIP: 07110 COMPUTER READABLE MEDIUM TYPE: PI COMPUTER: IBM IO OPERATING SYSTE SOFTWARE: PATE CURRENT APPLICATION NAME: PATE CLASSIFICATION NUM REFERENCE/DOCKET TELEFAX: (510) FORMATION FOR SEQ SEQUENCE CHARACTEI LENGTH: 28 base TYPE: NULLEICS: TOPOLOGY: Tine MOLECULE TYPE: DI TOPOLOGY: Tine MOLECULE TYPE: DI TOPOLOGY: Tine MOLECULE TYPE: DI TOPOLOGY: Tine MOLECULE TYPE: DI TOPOLOGY: Tine MOLECULE TYPE: DI TOPOLOGY: Tine MOLECULE TYPE: DI TOPOLOGY: Tine		
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h 100.0 Similarity 100.0 28; Conservative	1 38-928-2 38-928-2 38-928-2 RAL INFORMATION: PLICANT: TSANG, Sue Y. PLICANT: TSANG, SUE Y. PLICANT: TSANG, SUE Y. PLICANT: TSANG, SUE Y. PLICANT: TSANG, SUE Y. MER OF INVENTION: Oligonuc TLE OF INVENTION: HCV NUCL MERC OF SEQUENCES: 5 RRESPONDENCE ADDRESS: ADDRESSEE: Hoffmann-La Roc STREET: 340 Kingsland Stre CONTY: Nutley STATE: NJ ZIP: 07110 MPOTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatibl OPERATING SYSTEM: PC-DOS/M REDIUM TYPE: Floppy disk COMPUTER: IBM PC compatibl OPERATING SYSTEM: PC-DOS/M RECINTARTION NUMBER: US/08/ FILING DATE: CLASSIFICATION: REGISTRATION NUMBER: 35,32 REFERENCE/DOCKET NUMBER: 35,32 REFERENCE	•	00000000000000000
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OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Target
US-09-547-757-1
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                               Query Match
Best Local :
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                                                                                                                  LENGTH: 47
TYPE: DNA
ORGANISM:
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CURRENT FILING DATE: 2000-06-21
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NAME: Petry, Douglas A:
REGISTRATION NUMBER: 35,321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION NUMBER:
                                                                                                                                                                  PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                          Application US/09547757
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JM TYPE: Floppy disk

JTER: IBM PC compatible

XTING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                       GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                              GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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             Conservative
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                                                                                                                                                                                                                     MSI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roche Molecular Systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                  Detection and Amplification of RNA using
Target-Mediated Ligation of DNA by RNA Ligase
                       100.0%;
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N: MODIFIED NUCLEIC ACID AMPLIFICATION

N: PRIMERS...
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                    Score 28;
Pred. No.
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      Mismatches
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                    0.00013;
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                                                                           Sequence: Synthetic
                            Length 47;
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                        PITLE OF INVENTION:
                                                       APPLICANT:
                                                                      APPLICANT:
                                                                                                   APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy diskette
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                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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FILING DATE: '29 MAY 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                       54 GCAAGCACCCTATCAGGCAGTACCACAA 27
                                                                                                                                                                                                                                                                  Similarity
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               SEQUENCES:
                                                                                                                      Application PC/TUS9304863
                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                John J. Carrino
Joann C. Sustachek
ABBOTT LABORATORIES
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                                                                                             Ronald L. Marshall
                                                                                                                                                                                                                                                   Conservative
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Microsoft Word 5.1a
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Joann Sustachek
ADDRESS
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               AMPLIFICATION OF RNA SEQUENCES USING THE LIGASE CHAIN REACTION
                                                                                                                                                                                                                                                         100.0%; Score 28; DB 1; 100.0%; Pred. No. 0.00013;
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Abbott Laboratories

COUNTRY:

USA

Abbott Park

One Abbott Park Road

Illinois

60064-3500

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JS-09-034-205-37/c
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 5172.PC.01
TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, Kamrin T.
REGISTRATION NUMBER: 38,230
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MEDIUM TYPE: Floppy diskette
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                                                                                     APPLICATION NUMBER:
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5. 6194149
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                                                                                                                                                                                                                                     CA
                                                                                                                                                                                                                                                                 E: MEDLEN & CARROLL, LLP
220 Montgomery Street, Suite 2200
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TD NO: 36:
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                                                                                                                                                                                                                                                                                                                                                                    Neri, Bruce P.
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Pred. No. 0.
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Query Match Best Local Similarity

Matches

Conservative

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Indels

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Gaps

Score 28; DB 4; Pred. No. 0.00018; Mismatches

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US-08-934-097A-37/c
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                                              US-08-934-097A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION:
                                                                                                                                                                                                          REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FOI
TELECOMMUNICATION INFORMATION:
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                                                         MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,23
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IIILE OF INVENTION: Structure Probing With Structure-Bridging
IIILE OF INVENTION: Oligonucleotides.
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ZIP: 94104
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                                                                                         TOPOLOGY: linear
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220 Montgomery Street, Suite 2200
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                                                           /desc = "DNA" ·
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.00018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
            Length 232;
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                                                                                                                                                        patent No. 6355437
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 232 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION:
 CORRESPONDENCE ADDRESS:
                                                                                                        APPLICANT: Lyamichev, Victor I.
Brow, Mary Ann D.
                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                          1 GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                            h 100.0%; Score 28; DB 4;
Similarity :100.0%; Pred. No. 0.00018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVENTION: Polymorphism Analysis By Nucleic Acid INVENTION: Structure Probing | SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAGCACCCTATCAGGCAGTACCACAA 28
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Dahlberg, James
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/desc = "DNA"
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                                                                      Bruce P
                                   TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING OLIGONUCLEOTIDES
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Query Match
Best Local Similarity
""+ches 28; Conserva
                                                                                       ; LENGTH: 232
; TYPE: DNA
; ORGANIZM: Hepatitis C virus
US-09-677-192-37
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                                                                                                                                                              SEQ ID NO 37
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                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                  PRIOR FILING DATE:
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28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Lyamichev, Victor I. Brow, Mary Ann D.
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llarity 100.0%;
Conservative 0
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                               100.0%;
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                  Mismatches
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NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-03268
TELECOMMUNICATION INFORMATION: SEQUENCE DESCRIPTION: SEQ ID NO: 37: MOLECULE TYPE: other nucleic acid 1 GCAAGCACCCTATCAGGCAGTACCACAA 28 APPLICATION NUMBER: 09/034,205 FILING DATE: <Unknown> APPLICATION NUMBER: US/09/677,218B FILING DATE: 02-Oct-2000 CLASSIFICATION: <Unknown> MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, ADDRESSEE: MEDLEN & CARROLL, LLP STREET: 220 Montgomery Street, Suite 2200 Score 28; DB 4; Pred. No. 0.00018, ); Mismatches 0, Version #1.30 Gaps

CURRENT APPLICATION NUMBER: US/09/677,192
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/034,205 IITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING Score 28; DB 4; Pred. No. 0.00018; Length 232;

0;

Gaps

STREET:

220 Montgomery Street,

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US-09-034-205-32
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Best Local :
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                                                                                                                                       ENERAL INFORMATION:
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LENGTH: 239 base pairs
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MEDIUM TYPE: Floppy
                                                                                                                        APPLICANT:
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                                           ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid. STRANDEDNESS: double
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                              239 GCAAGCACCCTATCAGGCAGTACCACAA 212
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                                                                                                     Brow, Mary Ann D.
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                                                                                       Fors, Lance
                                                                                                                     Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 705-8410
415) 397-8338
MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     other nucleic acid
                                                                          Bruce P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamrin T.
ER: 38,230
                                           TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING OLIGONUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING OLIGONUCLEOTIDES
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Pred. No. 0.00018
; Mismatches 0
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US-09-034-205-36
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FOI
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                                                                                                            SOFTWARE: PatentIn Re-
CURRENT APPLICATION DATA
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
MEDLEN & CARROLL, LLP
TOTAL STREET, Suite 2200
                                                                                                                                                                                                                                                                                                                                     TITLE OF
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                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION:
ITLE OF INVENTION:
                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             האבטוד TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
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                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  Structure
Oligonucle
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                                                                                                                           Release #1.0,
                                                                                             US/08/934,097A
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   FORS-02980
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Pred. No. 0.0001
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                                                                                                                             Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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0;

TELEFAX: (415) 397-83

(415)

397-8338

239 base pairs cleic acid

TELECOMMUNICATION INFORMATION

(415)

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA";

linear

double

Match | 100.0%; Local Similarity 100.0%;

Score 28; DB 4; Length 239; Pred. No. 0.00018;

28;

Conservative

Mismatches

Indels

1 GCAAGCACCCTATCAGGCAGTACCACAA 28

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Query Match
Best Local Similarity
                            Matches
                                                                                                                                                                                                            TELEFAX: (415) 397-8338
NFORMATION FOR SEQ ID NO:
                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      NAME: MACKNIGHT, KAMPION:
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/M5-D00
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRESSEE
GCAAGCACCCTATCAGGCAGTACCACAA 28
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                                                                                                                                                           239 base pairs
                                                                                                                                                                                                                                                                                                                                                                   ION NUMBER: . US/08/934,097A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLEN & CARROLL, LLP
                                                                                                                                                   double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structure Probing With Structure-Bridging Oligonucleotides.
                                           100.0%;
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                                                                                                                                                                                                                                                                              FORS-02980
                                           Score 28; DB 4;
Pred. No. 0.00018;
                                Mismatches
                                                           Length 239;
                                 Indels
                                 0;
                                 Gaps
```

US-08-851-588-32

MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"

SEQUENCE CHARACTERISTICS: LENGTH: 239 base pairs TYPE: nucleic acid

STRANDEDNESS:

double

Query Match Best Local Similarity

100.0%; ilarity 100.0%; Conservative

0

Score 28; DB 4; Pred. No. 0.00018; Mismatches

. Length 239; Indels

0;

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239. GCAAGCACCCTATCAGGCAGTACCACAA. 212

1 GCAAGCACCCTATCAGGCAGTACCACAA 28

Search completed: July 10, 2003, 20:27:39 Job time: 12.5213 secs

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08-851-588-32/c
INFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ent No.
                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         TELECOMMUNICATION INFORMATION:
                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT:
                                                           REGISTRATION NUMBER: 40,027
                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                      COUNTRY:
                            TELEPHONE:
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                               LE OF INVENTION: Polymorphism Analysis By Nucleic Acid Designation: Structure Probing
                                                                                                                                                                                                                                                                                                                                                ESPONDENCE. ADDRESS:
                                                                                                                                                                                           ERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                   220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyamichev,
                                                                                                                                                                                                                                                                                                                                                                                                               Fors, Lance
                (415) 397-8338
                                                                                                                                                                                 Patentin Release #1.0,
                                (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Victor
                                                                                                                                                     US/08/851,588
                                                              FORS-02777
                                                                                                                                                                                     Version #1.30
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                    Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score: Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        greater
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28
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   is the number of results predicted by chance to have a ster than or equal to the score of the result being printed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/pubpna/US07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                    Length
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0 US-09-825-574-34
US-10-087-631B-13
US-10-087-631B-13
US-10-087-631B-13
US-09-825-574-27
0 US-09-825-574-28
0 US-09-825-574-29
0 US-09-825-574-31
US-09-940-925A-123
US-09-940-925A-125
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US-09-870-939-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pubpna/US06_NEW_PUB.seq: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pubpna/PCTUS_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /pubpna/US09_PUBCOMB.seq:*
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576.891 Million cell updates/sec
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                                                                                                                                      Sequence 13,
Sequence 13,
Sequence 15,
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Sequence
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Appli
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                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/087,631B
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-087-631B-7
                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10087631B Publication No. US20030054372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                                Local
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
366	347	341	341	341	315	298	289	289	289	286	282	282	282	282	281	281	281 .	281	281	281	281	281	281	281	281
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US-09-992-160-48	US-10-132-295-1	US-09-814-292-44	US-10-259-275-35	US-09-814-357-3	US-09-345-761-6	US-09-345-761-7	-09-825-574-		US-09-825-574-20	US-09-825-574-21	US-09-941-193A-130	US-09-941-193A-124	US-09-940-925A-130	US-09-940-925A-124	-941-193A-	·941-193A-	US-09-941-193A-129	US-09-941-193A-128	US-09-941-193A-126	US-09-941-193A-125	US-09-941-193A-123	US-09-940-925A-132	US-09-940-925A-131	US-09-940-925A-129 '	US-09-940-925A-128
Sequence 48, Appl	Sequence 1, Appli	Sequence 44, Appl	Sequence 35, Appl	Sequence 3, Appli	6,	7,	Sequence 23, Appl	22,	20,	Sequence 21, Appl	130,	124,	130,	124,	•	•	•	Sequence 128, App	•	•	•	•	Sequence 131, App	•	Sequence 128, App

## ALIGNMENTS:

```
RESULT 2
US-09-870-939-1/c
                                                                              Sequence 1, Application US/09870939 Publication No. US20020192650A1 GENERAL INFORMATION:
                       APPLICANT: AMORESE, DOUGLAS A. APPLICANT: SHANNON, KAREN W. APPLICANT: COLLINS, PATRICK J. APPLICANT: WOLBER, PAUL K.
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative
10010791-1
           COMPOSITE ARRAYS
                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                      Score 28; DB 9;
Pred. No. 0.00081;
); Mismatches 0;
                                                                                                                                                                                                                                                                  Length 28
                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                         0;
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Os-09-825-574-37 DESCRIPTION: desc _ "DNA"  Ouery Match Best Local Similarity 100.0%; Score 28; DB 10; Length 232;  Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ROLL, LLP Street, Suite 22 1e MS-DOS #1.0, Version 1825,574	CURRENT APPLICATION NUMBER: US/09/870,939  COURRENT FILING DATE: 2001:10-12  SOFTWARE: PSQ ID NOS: 1001:10-12  SED IN NO: 1 Patentin Ver 2.1  LENGTH NO 1 Fatentin Ver 2.1  LENGTH NO 1 FATENTIN VER 2.1  LENGTH NO 1 FATENTIN VER 2.1  ORGANISM: Hepatitis C virus  OUS 9870-939-1 100.0%; Score 28; DB 9; Length 60;  OUS 109-870-939-1 100.0%; Score 28; DB 9; Length 60;  DO 1 GCAGCCCCTATCAGGCAGTACCACAA 20  STULT 3 SMILLIFIT 11111111111111111111111111111111111
Oy  1 GCAAGCACCCTATCAGGCAGTACCACAA  28; CONSERVALIVE  1 GCAAGCACCCTATCAGGCAGTACCACAA  29   1	YOUNG TO THE ACTION IN THE STATE OF THE STAT	Qy  1 GCAAGCACCCTATCAGGCAGTACCACAA 28  Db  23

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DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-825-574-36
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-825-574-33/c
                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/09825574
Patent No. US20020119454A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                               APPLICANT: Lyamichev, Victor I.
Brow, Mary Ann D.
Fors, Lance
Neri, Bruce P.
TITLE OF INVENTION: Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
Structure Probing With Structure-Bridging
Oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-8
MATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 GCAAGCACCCTATCAGGCAGTACCACAA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                    STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MacKnight, Kamrin T. REGISTRATION NUMBER: 38,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/825,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               COUNTRY: USA
                                                                                                   STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FORS-02980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/934,097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Structure Probing With Structure-Bridging
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Pred. No. 0.0
0; Mismatches
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RESULT 7
US-09-825-574-34/c
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Best Local Similarity 100.
---- 28; Conservative
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Patent No. US20020119454A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: THM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
            ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
Structure Probing With Structure-Bridging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lyamichev, Victor
Brow, Mary Ann D.
Fors, Lance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/825,574
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 GCAAGCACCCTATCAGGCAGTACCACAA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>
                                                                            APPLICATION NUMBER: 08/934,097 FILING DATE: <Unknown>
                                                                                                                                     APPLICATION NUMBER: US/09/825,574 FILING DATE: 03-Apr-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FORS-02980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/934,097 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
REFERENCE/DOCKET NUMBER: FORS-02980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neri, Bruce P.
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Pred. No.
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INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:

TELEFAX:

(415)

TELEPHONE:

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SEQUENCE DESCRIPTION: US-09-825-574-35
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        MOLECULE TYPE: other nucleic acid
| DESCRIPTION: /desc = "DNA"
| SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: /desc = "DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
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                                                                       LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/934,097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ER OF SEQUENCES:
                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FORS-02980
                                                                                                                                                                                                                        NAME: MacKnight, Kamrin T. REGISTRATION NUMBER: 38,230
                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/825,574 FILING DATE: 03-Apr-2001
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            ELEPHONE:
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                                                                                                                                            FOR SEQ ID NO: 35
                                                                                                                         CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 Montgomery Street,
                                                                                                                                                           (415)
 /desc
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                                                                                                                                                              397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism Analysis By Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure Probing With Structure-Bridging
                                                                                                                                                                                                                                                                                                                                                                                       Release #1:0,
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
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                                                                                                                                                 ; OTHER INFORMATION: Description of artificial sequence: Amplicon sequence derived ; OTHER INFORMATION: QS HCV (HCV amplification control having binding sites for ST2; OTHER INFORMATION: and ST2535) using primers ST280 and ST778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-087-631B-13/c
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US-10-087-631B-10/c
                                                                                          Query Match
Best Local Similarity
                                                                          Matches
                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/10087631B Publication No. US20030054372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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LENGTH: 241
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                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JAEGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING TITLE OF INVENTION: CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                         ORGANISM:.Artificial Sequence
                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                  ENGTH: 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
241 GCAAGCACCCTATCAGGCAGTACCACAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GCAAGCACCCTATCAGGCAGTACCACAA 214
                                                                          28;
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                                   1 GCAAGCACCCTATCAGGCAGTACCACAA 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description of Artificial amplification of HCV type
                                                                                        100.0%;
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                                                                                        Score 28; DB 9;
Pred. No. 0.001;
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Pred. No. 0.001;
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                                                                        Mismatches
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                                                                                                       DB 9; Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence: DNA sequence derived.
1 using primers ST280 and ST778
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Query Match

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DB 10;

Length 240;

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US-09-825-574-26/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/087,631B
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JAEGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quence 26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 242
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                             INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GCAAGCACCCTATCAGGCAGTACCACAA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              NAME: MacKnight, Kamrin T. REGISTRATION NUMBER: 38,230
                                                                                                                                                                                                                           APPLICATION NUMBER: 08/934,097 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/825,574 FILING DATE: 03-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
                                                                                                                                           REFERENCE/DOCKET NUMBER: FORS-02980
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                              TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                     ENGTH: 244 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09825574
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Brow, Mary Ann D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description of artificial sequence: Amplicon derived from HCV (HCV-specific amplification control) using ST280 and
                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism Analysis By Nucleic Acid
Structure Probing With Structure-Bridging
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Pred. No. 0.
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0.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DESCRIPTION: /desc = "DNA"; SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-09-825-574-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-825-574-27/c
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Matches
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Best Local Similarity
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                                                                                                 Local
                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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TELEPHONE: (415) 705-8410
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
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DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
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241 GCAAGCACCCTATCAGGCAGTACCACAA 214
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                                      1 GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                 Similarity
                                                                                                                                                                                                                                                             LENGTH: 244 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MacKnight, Kamrin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
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Structure Probing With Structure-Bridging
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Brow, Mary Ann D.
Fors, Lance
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                                                                                               100.0%; Score 28; 100.0%; Pred. No.
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9

Gaps

0

Sequence 28, Application US/0982574
Patent No. US20020119454A1
GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200

ITY: San Francisco

USA

NUMBER OF SEQUENCES:

TITLE

Lyamichev, Victor I.
Brow, Mary Ann D.
Fors, Lance
Neri, Bruce P.

OF INVENTION: Polymorphism Analysis By Nucleic Acid Structure Probing With Structure-Bridging Oligonucleotides.

ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,

Version #1.30

APPLICATION NUMBER: US/09/825,574
FILING DATE: 03-Apr-2001
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: 08/934,097 FILING DATE: <Unknown>

-09-825-574-28

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                                                                                                                   Sequence 29, Application US/09825574.
Patent No. US20020119454A1
GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MACKNIGHT, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
TELECOMMUNICATION INFORMATION:
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid Structure Probing With Structure-Bridging Oligonucleotides.

Oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                         APPLICANT: Lyamichev, Victor I.
Brow, Mary Ann D.
                                                                                                                                                                                                                     241 GCAAGCACCCTATCAGGCAGTACCACAA 214
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28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 244 base pairs
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                                                                                                                                                                                                                                                                                Conservative
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100.0%; Pred. No. 0.001;
tive 0; Mismatches
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Search completed: July 11, 2003, 15:01:57 Job time: 77.6382 secs
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                                                                                                                                            Matches
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                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: FORS-02980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/934,097
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                                                                                                                                                                                                                                                                                                     LENGTH: 244 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MacKnight, Kamrin T. REGISTRATION NUMBER: 38,230
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100.0%; Pred. No. 0.0
ative 0; Mismatches
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BH101607 RPCI-24-2

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BG070203 H3084G10BG953300 CM4-CT062
BE558358 HV\_CEB0011
AL410827 T7 end of
A1151927 u147h03.y
BQ523467 NISC\_n122A290946 RPCI-24-1
AL643408 AL643408
BG721879 602694496
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Result
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length: 2000000000
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Match
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28
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DEFINITION
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 572)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                      Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas018o13.sp6
Sequencing primer: SP6
                                                                                                                                                                                                                                                                mRNA sequence.
AL633783
                                Sequencing primer: SP6
This sequence is from a Xenopus
constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                     AL633783 XGC-gastrula Silurana tropicalis cDNA clone TGas018013 5',
                                                                                                                                                                                                                               western clawed frog.
                                                                                                                                                                                                                                                      AL633783.1 GI:16603266
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71.4
71.4
71.4
71.4
71.6
68.6
68.6
67.9
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1. .572
/organism="Silurana tropicalis"
             Location/Qualifiers
1. .572
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0 BI78052.

BI780522

7107546
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AW735854 EST336622
BI052510 PM3-GN030
AI959681 fd12908.x
BF218410 601881771
BH534982 BOHKL10TR
AW448341 BXY\_587 B
BQ609725 BXY\_587 W
BG855643 102403460
BF128397 501810288

T95529 ye46e09. AI032822 ox17f05 AL036499 DKFZp56 AI553272 v126d07 AV255262 AV25526

ox17f05.

5262 AV255262

B1780523 EBes01\_SQ B1780522 EBes01\_SQ BJ075404 BJ075404 BH866052 SALK\_1006 BH861324 SALK\_0679 BG893014 daa92912. AQ168839 HS\_3212\_B AW643816 Cm34b12.W BE118249 UT-R-B51-BM290110 EST576644

Gene Collection (XGC) library

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RESULT 3
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                           32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           western clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AL637026
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                                                                                                 GCAAGCAGCCTCTCAGGCACCACCACAA 59
                                                                                                                                                         GCAAGCACCCTATCAGGCAGTACCACAA 28 · ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROPICALIS_SEQUENCE_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iail: trop@sanger.ac.uk
inger Xenopus tropicalis EST project 2001
ioPICALIS_SEQUENCE__D: TNeu004n20.sp6
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ECORI-NOTI cut CDNA was then ligated
ECORI at the 5' end and NOTI at the 3
194 c 129 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="xGC-neu._
clone_lib="xGC-neu._
dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; /note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; /note="vector: pCS107 site_1 into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neurula into pCS107 with or neur
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'clone="mw-----
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                                                                                                                                                                                                                                                                                                                  77.1%;
85.7%;
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                                                                                                                                                                                                                                                                                                     Score 21.6;
Pred. No. 55;
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Pred. No. 5
                                                                                                                                                                                                                                                               Mismatches
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ia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                       Length 585;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanger Xenopus tropicalis EST project 2002

Contact. T. Croning, M.D.R., Zorn, A.M. and Rogers, J. Contact. T. Croning, M.D.R., Zorn, A.M. and Rogers, J. Contact. T. Contact. T. Contact. T. Contact. T. Contact. T. Contact. T. Croning, M.D.R., Zorn, A.M. and Rogers, J. Contact. T. Croning, M.D.R., Zorn, A.M. and Rogers, J. Contact. T. Croning, M.D.R., Zorn, A.M. and Rogers, J. Croning, M.D.R., Zorn, A.M. and Rogers, Croning, M.D.R., Zorn, C. Croning, M.D.R., Zorn, C. Croning, M.D.R., Zorn, C. Croning, M.D.R., Zorn, A.M. and Rogers, C. Croning, M.D.R., Zorn, A.M. and Rogers, C. Croning, M.D.R., Zorn, C. Croning, M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing primer: P1CSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TROPICALIS_SEQUENCE_ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinxton,
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                                                                                                                                                                                                                                                                                                                                                    182
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                /lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cl
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cl
was oligo dT primed from 5ug of poly A+ RNA from neuri
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
205 c 137 g 95 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="XGC-neurula"
/dev_stage="neurula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="TNeu111121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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                                                                                                                                                                 77.1%;
85.7%;
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                                                                                                                                                            Score 21.6;
Pred. No. 56;
                                                                                                                    Mismatches
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TNeullli21.plcSP6
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ia; Pipoidea;
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; Pipidae;
                                                                                                           0
                                                                                              Gaps
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Matches 61: GCAAGCAGCCTCTCAGGCACCACCACAA 88

DEFINITION mrnA linear EBro08\_SQ002\_B06\_R root, 3 week, drought-stressed, Hordeum vulgare cDNA clone EBro08\_SQ002\_B06\_5', mR EST. BI777787.2 GI:21951028 BI777787 fordeum vulgare. cv Optic, EST 23-JUL-2002 PV Optic, EBro08

TITLE JOURNAL Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scr Genome Dynamics/Computational Biology On Sep 26, 2001 this sequence version Contact: Waugh R, Marshall Dr On Sep 26, 2001 th 1 (bases 1 to 306)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Hordeum vulgare Triticeae; DD2 5DA, Scotland, replaced gi:15780679. Ŗ Embryophyta; Tracheophyta; a; Poales; Poaceae; Pooideae

닭 Ş

FEATURES

All Seq

> 00 44 1: 1: est@sc sequence

primer: M13 reverse.

has a Phred quality score of 20

or over

Location/Qualifiers

Email: est@scri.sari.ac.uk

44 1382 562426

source

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572 GCAAGCTCCCGAACAGGCAGTACCAC

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BASE COUNT
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Best Local
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                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271. GCAAGCTCCCGAACAGGCAGTACCAC 246
1 GCAAGCACCCTATCAGGCAGTACCAC
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum
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                                                                                                                                                                                                                                                 Institute of Arable Crop Research
Long Ashton, Bristol BS41 9AF United Kingdom.
                                                                                                                                                                                                                                                                               Contact: Barker G
                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                     bread wheat.
                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 593)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4565"
/clone="pl0_j223_plate_11"
/clone_lib="j:223"
/tissue_type="embryo"
/tissue_type="embryo"
/dev_stage="21 days post anthesis"
211 c 192 g 110 t
                                                                                                                                                                                             /organism="Triticum aestivum"
/cultivar="mercia"
                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Hordeum vulgare"
/cultivar="Optic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'dev_stage="3 week"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:21829654
                                                                                                                                                                                                                          . 593
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                                                      75.7%;
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88.5%;
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Pred. No. 62;
                                                        Score 21.2;
Pred. No. 8
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                                         Mismatches
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                                                        82;
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                                                                     BB
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                                                                                                                                                                                                                                                                                                         the academic community
                                                                                                                                                                                                                                                                                                                                   Lenton, J.,
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••
                                                                                                                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooideae
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                                                                  Length 593;
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J., Shewry,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: oandersn@pw.usda.gov
Sequences have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, C. and Woo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Crossman, C., Fenton, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 731)
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                                                                                                                                                                                                                                             20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 20, 24, 28, 30 DPA and total RNA was prepared by Altenbach and K. Cronin at USDA-ARS, Albany, CA. library was made using poly (A) RNA, and the cDNA were in vivo excised to give pBluescript SK(-) phag in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside Plasmid DNA
                     Anderson
228 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Environment 3) 370C/17oC day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/17oC day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370C/17oC day/night plus drought, with
                                                                 preparations and DNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                      post-anthesis fertilizer, Environment 6) 37oC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             well-watered, without post-anthesis fertilizer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
ScoRI; Plants were grown under six following different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'tissue_type="whole grains
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//17oc day/night, well-watered, with post-anthesis
illizer, Environment 2) 24oc//17oc day/night,
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grains cDNA library Triticum
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                                                                                                462
                                                                                                                                                                  73.6%;
Similarity 85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html seq primer: SP6 clumn: 3
                                                                                 CAAGCACCCTAGCATGCGTTACCACAA 436
                                                                                                       CAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onpublished (1999)
Other_GSSs: RPCI-24-229K3.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 482)
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BH101607
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                                                                                                                                                                                                                                                 /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPC1-24 Mouse BAC tibrary produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="RPCI-24-229K3"
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
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88.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missouri (web address; www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1.7.)
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Un, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B. Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, T., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, T., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, T., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, T., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, T., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, N., Schurk, R., Ritte, M., Libbons, M., Pape, D., Harvey, M., Schurk, R., Ritte, M., Libbons, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'fc23e12.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3772254 5' similar to SW:YB4F_SCHPO 014360 HYPOTHETICAL 57.6 KD PROTEIN C30D10.15 IN CHROMOSOME II. ; mRNA sequence.
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                                                                                                                                   sites of the psport vector (BR). Library was constructe by Matthew Clark (Lehrach lab; ICRF, London and Max Planc Institut fuer Molekulare Genetik, Berlin), cDNAs for EST mybridization fingerprinting of arrayed clones from embryonic shield stage (5 6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were
                                                                                                   sequenced to assess clustering parameters or single clones
                                                                                          were sequenced additional times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: psport1; Site_1: Not1; Site_2: Sal1; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'psacTagTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT]'];
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double-stranded cDNA was ligated to Sal I adaptors (Bidigested with Not I and cloned into the Not I and Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stage embryos"
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/db_xref="taxon:7955"
/clone="IMAGE:3722254"
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                                                                        to assess quality
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,R., Ritter,E.,
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1 GCAAGCACCCTATCAGGCAGTACCACAA 28

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Score 20; I Pred. No. 2.

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Mismatches

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                                                                                                                                                  Query Match
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501 GCTAGCACCCTCTAAGGCAGATCCACAA 528
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H3084G10-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3084G10 5', mRNA sequence.
                                              1 GCAAGCACCCTATCAGGCAGTACCACAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institute on Aging/National Institutes of Health 333 cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please Visit http://lgsun.grc.nia.nih.gov/CDNA/15k.html for details. Plate: H3084 row: G column: 10
Seq.primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Other_ESTs: H3084G10-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: George J. Kargul 
Laboratory of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                 MOL
                                                                                                                                                                                                                                                                                                                                                                )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000,
                                                                                                                                                                                                                                                                                             unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: psport1; Site_1: Sal1; Site_2: Not1; This clone is among a rearrayed set of 15,47 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos.
                                                                                                                                                                                                                                                                                                                                              patterns during preimplantation mouse develo
Development, 127: 1737-1749; (3) Genome-wide
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/strain="C57BL/6J"
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'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="NIA Mouse 15K cDNA Clone Set"
sex="Clones arrayed from a variety of cDNA libraries"
dev_stage="Clones arrayed from a variety of cDNA
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                                                                                                                                                                                                                        under-representation on the Genet 7: 1967-1978."
177 c 112 g 163 t
                                                                                                                      71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E12.5 female mesonephros/gonad) and one newborn cDNA library. Average insert size 1.5 kb. All e libraries are cloned unidirectionally with Oligo(dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         host="DH10B"
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                                                                                                                      Score 20;
Pred. No.
                                                                                                 Mismatches
                                                                                                                      DB 12;
2.7e+02;
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H3084G10-3 NIA Mouse 15K CDNA
H3084G10 3', mRNA sequence.
BG070203
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                                                   Unpublished (2001)
Other_ESTs: H3084G10-5
                                                                                   Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K.,,T.S., Carter,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU117139 HEMBAl Homo sapiens
                   Contact: George J. Kargul 
Laboratory of Genetics
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 827)
                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genomics@hri.co.jp
HRI human cDNA project; 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1532-3 Yana, Kisarazu,
Tel: 81-438-52-3975
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Unpublished (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AU117139
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National Institute on Aging/National Institutes of Health
                                                                                                                                                                                                           house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole embryo, m
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
182 c 185 g 225 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="HEMBA1000758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
82.18;
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A Clone
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                                                                                       NIA mouse
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                                                                                                                     Jaradat, S.A., Tanaka
                                                                                       15K
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                                                                                                                                                                                                                                                                                 cDNA clone
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FEATURES

Source

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Dias Neto,E., Garcia correa,R
Nagai,M.A., da Silva,W. Jr.,
                                                                                                                        Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                           sequence tags
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                 Homo sapiens
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EST.
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CM4-CT0629-220101-700-g09 CT0629 Homo sapiens cDNA, mRNA sequence.
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This clone set has been freely distributed to the community. please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
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                                                                         tgun sequencing of the human transcriptome with ORF
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,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.

, B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patterns during preimplantation mouse development Development, 127: 1737-1749; (3) Genome-wide maps unselected transcripts from extraembryonic tissue 7.5-day mouse embryos reveals enrichment in the and under-representation on the x chromosome, 19. Mol Genet 7: 1967-1978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression profiling of mid-gestation placenta and ensing a 15,000 mouse developmental cDNA microarray, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene exprese patterns during preimplantation mouse development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(drexpression profiling of mid-generation.) Genome-wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn
                                       Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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/strain="C57BL/6J"
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/db_xref="taxon:10090"
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82.1%;
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Pred. No. 3.1e
0; Mismatches
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                      EST 12-JUN-2001
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BE558358
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Seg primer: AATTAACCCTCACTAAAGGG
                                 Email: rwing@clemson.edu
Total hq bases = 113
                                                                                                                                                                                                            Unpublished
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MEDLINE JOURNAL TITLE

DEFINITION ACCESSION

VERSION KEYWORDS

RESULT 1: BG953300

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Matches Query Match

Local

BASE COUNT

REFERENCE

ORGANISM

AUTHORS

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Clemson University
100 Jordan Hall, C
Tel: 864 656 7288
Fax: 864 656 4293
                                                                           Clemson University Genomics Institute
                                                                                                        On Aug 14, 2000 t
Contact: Wing RA
                                                                                                                                                               Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi D.W., Fenton, R.D., Oates, R. and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mia6) seedling
                                                                                                                                                                                                                                                                                                             Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                          1 (bases 1 to 828)
Wing, R., Close, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            BE558358.2 GI:13265876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV_CEb0017F16f Hordeum vulgare seedling g
HVcDNA0005 (Blumeria challenged) Hordeum
HY_CEb0017F16f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare.
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Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM4&t2=CM4-CT0629-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mail: asimpson@ludwig.org.br
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+55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 19, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue stringency conditions."

Stringency conditions."

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/clone_lib="CT0629"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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84.6%;
                                                                                                           this sequence version replaced gi:9822848
                                  Clemson, SC 29634, USA
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Prudente 109, 4 andar, 01509-010,
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Pred. No. 2.7e+02;
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Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                      Bolotin-Pukuhara,M., Boń,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalggeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
                                                                                                                                                                                                                                                                           Yarrowia lipolytica.
Yarrowia lipolytica
                                                                                                                                                                                                                                                                                                                                                                         Yarrowia lipolytica,
AL410827
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                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                   AL410827.1 GI:12179594
                                                                                                                                                                                    Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.
                                                                                                                                                                                                                                  Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.I. 16151 (Mla6) plants were greenhouse grown in the Wise lab at Iowa State University, Ames, IA; 7 day old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
241 c 215 g 171 t 1 others
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/cultivar-"CI16151 (Mla6)"
/db_xref-"taxon:4513"
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/clone_lib="Hordeum vulgare seedling green leaf EST
ibrary HVcDNA0005 (Blumeria challenged)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    host-"SOLR"
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Pred. No. 6.9e+02;
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3 AAGCACCCTATCAGGCAGTACCACAA 28
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387 AAGCACTTTGTCARGCAGTACAACAA 362
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475 bp mRNA linear u147h03.yl Sugano mouse embryo mewa Mus musculus IMAGE:1885589 5', mRNA sequence.
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This GS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii.
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                                                                                                                                          1 (bases 1 to 475)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angusta, Debaryomyces hansenli var. hansenli, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage. 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Casaregola, S., Neuveglise, C., Artiguenave, F., Wincker, P. an
                                                           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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the other extremity of this insert.
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                                                                                                                    Theising, B., Wylie, T., Lennon, G.,
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/note="similar to Saccharomyces
KARZ; nuclear fusion protein ]
1 putative frameshift(s)"
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/clone="aWOAA007B06"
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Pred. No. 7.4e+02;
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and Gaillardin,C.
hemiascomycetous yeasts: 17. Yarrowia
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Search completed: July 11, Job time: 511.434 secs	Query Match Best Local Matches  Qy  Db  341	BASE COUNT ORIGIN		FEATURES SOUTCE
Pleted: July 11, 2003, 02:25:58	Similarity 87.9%; Score 19; DB 9; Length 475; 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0; 1 GCAAGCACCATTATCAGGCAGTACCACA 27 1 GCAAGCACCATGACAGCCAGGACCACA 367.		i o o	Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:969913 Seq primer: custom primer used High quality sequence stop: 450. Location/Qualifiers 1, 475

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:
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## ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AP005640 .	RESULT 1
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	CIONE: USJNBAUUU6U15. Oryza sativa (japonica cultivar-group)	Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,	HTG; HTGS_PHASE2.	AP005640.1 GI:22266684	AP005640	OSJNBa0006015, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Oryza sativa (japonica cultivar-group) chromosome 2 clone	AP005640 139534 bp DNA linear HTG 16-AUG-2002		

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JOURNAL REFERENCE
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                                                                 Shaull, S., Lin, S., Dixon, R., Cook, D., Kim, D. and Roe, B.A.
                                                        Direct Submission
                                                                                                                               Submitted (23-MAY-2002) Department Of Chemistry
The University Of Oklahoma, 620 Parrington Oval,
                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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Pel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission |
Submitted (15-AUG-2002) Takuji Sasaki, National Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yrobiological Sciences, Rice Genome No. 1-2. Tsukuba, Ibaraki 305-8602, Japan
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          Department Of Chemistry And Biochemistry, oma, 620 Parrington Oval, Room 208, Norman,
                                                                             May, G., Sumner, L.,
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                                                                           Gonzales, B.,
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                                                                                                                                                                                                                                                                      Gonzales, B.,
                                                                                                                       Room 208, Norman
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On Jul 18, 2002 this sequence version replaced g1:21747483.
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Direct Submission
Submitted (01-AUG-2002) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Aug 1, 2002 this sequence version replaced gi:22002170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Walliams, G., Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Walliams, G., Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Walliams, G., Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Walliams, G., Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Walliams, G.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratlsson, E., Kelly, S., Khan, U., King, L., Lewis, L.C., Lewis, L.C., Liu, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Ma, J., Lucier, R., Lucier, R., Luna, R., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Metzker, M., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Med, G., Metzker, M., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Moser, M., Nguyen, A., Nguyen, N., Ngu
Submitted (07-MAR-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine,
                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                       Unpublished
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Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Fran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scherer, S., Scott, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Brya
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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l,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
l,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 145424 bp DI norvegicus clone CH230-334N2,
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     David, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bryant, N.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Banks, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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REFERENCE AUTHORS TITLE

Worley, K.C. Direct

Submission

Baylor Plaza,

(bases

1za, Houston, 1 to 145424)

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COMMENT

Baylor Plaza, Ho On Jul 12, 2002

Center: Baylor Co Web site:

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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 40 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: phrap; version 0.990329
Consensus quality: 118496 bases at least 0.40
Consensus quality: 121465 bases at least 0.30
Consensus quality: 123679 bases at least 0.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summary Statistics
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1 (bases 1 to 198868)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M.,
                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                           Norway rat.
Rattus norvegicus
                                            Kattus.
                                                                                                                            Rattus norvegicus clone CH230-126C16, ***, 58 unordered pieces.
                                                                                                  HTG; HTGS_PHASE1.
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NOTE:

is not known and their order in this sequence record is arbitrary. Gaps between the contist represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

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Submitted (12-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baylor Plaza,
On Jul 14, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baylor Plaza, Houston,
3 (bases 1 to 198868)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorrell, J.H., Guevara, W., Gunaratne, P., Hale, S
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NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 58 contigs. The true order of the pieces
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heshwari,M., Mapua,P., Martin,R., Martindale,A., Mart:
                                                                                                                                           Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149939 bases at least 040
Consensus quality: 156891 bases at least 030
Consensus quality: 162963 bases at least 020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
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Mawhiney, E., McLeod, M.P., Meador, M., Me
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Boatin, C.,

Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Stange-Thoman, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella, Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Geraigery, K., Gilmartin, T., Grant, G., Gardyna, S Depayre, E.,

Submitted (05-JUN-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 5, 1998 this sequence version replaced 91:3168631. Smit, A.F.A. &

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On Jul 16, 2000 this sequence version replaced gi:7940422.
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ACO19148 212030 bp DNA linear HTG 19-JUL-2000 Homo sapiens chromosome 17 clone RP11-772K16, WORKING DRAFT SEQUENCE, 15 unordered pieces. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. HTGS\_PHASE1; HTGS\_DRAFT.

The sequence of Homo sapiens clone

Louis,

Center: Washington University Genome Sequencing Center Center code: WUGSC

Insert size: 258000; Insert size: 210630;

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Quality coverage: 4.30 in Q20 bases; agarose-fp Quality coverage: 4.57 in Q20 bases; sum-of-contigs
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                                                                   /note="assembly_name:Contig10
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Trypanosoma cruzi strain ESMERALDO cl3 trypanothione reductase
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           'TLANSLATION-"TLYKKRVAVIDVOMVHGPPFFSALGGTCVNVGCVPKKLMVTGAO
'MEHLRESAGGGWEEDRTTLRAEMKKLIAVKDEAVLNINKSYEEMERDYEGLEEFLGW
'SLESKNVVNVRESADPASAVKERLETENILLASGSWPHMPNIPGIEHGISSNEAFYL
                                                                                                                                                                                                                              /organism="Trypanosoma
/strain="ESMERALDO cl3"
/db_xref="taxon:5693"
                                                                                product="trypanothione reductase"
protein_id="AAK71210.1"
                                                                                                                                                    product="trypanothione reductase"
                                                                                                                                                                              gene="TR
                                                                                                                                                                                                        gene="TR
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                                                                                                                 codon_start=]
                                                                                                                                                                                                                                                                                                                                                          and Ayala, F.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Ayala, F.J
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48441 c 49876 g 54852 t
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clone="RP11-772K16"

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                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-MAR-2001) Ecology and Evolutionary Biology, University of California, Irvine, 321 Steinhaus Hall, Irvine, 92697-2525, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequences provide evidence of genetic exchange among distantly related lineages of Trypanosoma cruzi Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7396-7401 (2001)
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Machado, C.A. and Ayala, F.J.
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Wachado, C.A. and Ayala, F.J.
                                                 Similarity
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CGTCTTTCGCAGATCGGTACC 21
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VMIKNGCVQVDEYSRTAVSNIYAIGDVRNRVMLTPVAINEAAALVDTVPGTNPRKTDH
TRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHNISGSKYKTFVAKIIT
NHSDGTVUGVHLLGDNAPEIIQCVGICLKLNAKISDFY°
3 318 c 353 g 310 t
                                                                                                                   TRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHNISGSKYKTFVAKIIT
NHSDGTVLGVHLLGDNAPEIIQGVGICLKLNAKISDFY"
1318 c 353 g 310 t
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                                                                                                                                                                                         TANGIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAIGRSPRTKDLQLQNAG
                                                                                                                                                                                                        PEPPRRVLTVGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGFDHTLREELTKQL
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YMEHLRESAGFGWEFDRTTLRAEWKKLIAVKDEAVLNINKSYEEMFRDTEGLEFFLGW
                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TR"
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1290)
Machado, C.A. and Ayala, F.J.
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Machado, C.A. and Ayala, F.J.
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Trypanosoma; Schizotrypanum.
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318 c 353 g 310 t
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TANGIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAIGRSPRTKDLQLQNAG
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/strain="CBB cl3"
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AF358997/c
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                                                                                                                                                                                      Trypanosoma cruzi
                                                                                                                                                                                                       Trypanosoma cruzi.
                                                                                                                                                                                                                                                   AR358997 1290 bp DNA
Trypanosoma cruzi strain SO3 cl5 haplotype
                                                                                                                                                                                                                                  AF358997.1 GI:14600031
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                        CGTCTTTCGCGGATTGGTACC
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                                                           leotide sequences provide evidence of genetic exchange among tantly related lineages of Trypanosoma.cruzi
                                                                                                                                                             /panosoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequences provide evidence of genetic exchange among distantly related lineages of Trypanosoma cruzi Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7396-7401 (2001)
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                                                                                                                                          (bases 1 to 1290)
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Trypanosoma; Schizotrypanum.
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Trypanosoma cruzi
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 A. and Ayala, F.J.

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PEPPRRVLTVGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGEDHTLREELTKQL
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                                                                                                                                                 Schizotrypanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="trypanothione reductase"
protein_id="AAK71213.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="TR
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                                                                                                                                                                Kinetoplastida;
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2 trypanothione
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University of California, Irvine, 321 Steinhaus Hall, Irvine,
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                                                                                                                                                                                                       Nucleotide sequences provide evidence of genetic exchange distantly related lineages of Trypanosoma cruzi Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7396-7401 (2001)
                                                                                                                                       Direct Submission
                                                                                                                                                    2 (bases 1 to 1290)
Machado, C.A. and Ayala, F.J.
                                                                                                                                                                                                                                                                                                 Trypanosoma cruzi,
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                               Trypanosoma; Schizotrypanum.
1 (bases 1 to 1290)
Machado, C.A. and Ayala, F.J.
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                                                                                                                                                                                                                                                                                                                                                                                                   (TR) gene,
AF358999
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19; Conserv
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/db_xref="taxon:5693"
/haplotype="2"
                            /strain="PSC-O"
                                      ∕organism="Trypanosoma
                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="Tlykkrvavidvonvhgpppfsalggtcvnvgcvpkklmvtgaq
xmehlresacfgredrttlrækkllavkdeavlninksyeemfrdeglefplgw
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90.5%;
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Length 1290;

Indels

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trypanothione

INV 05-JUL-2001

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Trypanosoma cruzi strain CL F11F5
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                                                                                                                                                                                                                                                                                                                    Submitted (12-MAR-2001) Ecology and Evolutionary Biology, University of California, Irvine, 321 Steinhaus Hall, Irvine,
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Trypanosoma; Schizotrypanum.
1 (bases 1 to 1290)
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Machado, C.A. and Ayala, F.J.
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/gene="TR"
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/strain="CL F11F5; CL Brener"
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Pred. No. 3
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Trypanosoma cruzi
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/db_xref="taxon:5693"
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YMEHLRESAGFGWEFDRTTLRAEWKKLIAVKDEAVLNINKSYEEMFRDTEGLEFFLGW
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ymehlreskafgwefprtlkaewkkijavkdeavlminksybemfroteglepflgw
gslesknvvnvresadpasavkerleteniillasgswphmpnipgibhcissnbafyl
                                                      VMIKNGGVQVDEYSRTNVSNIYAIGDVTNRVMLTPVAINEAAALVDTVFGTNPRKTDH
TRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHNISGSKYKTFVAKIIT
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## ALIGNMENTS

## RESULT 1 ABL30111 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds. Drosophila melanogaster genomic polynucleotide SEQ ID NO 41806. 26-MAR-2002 ABL30111; ABL30111 standard; DNA; (first entry) 768 BP.

Drosophila melanogaster.

WPI; 2001-656860/75. 23-MAR-2000; 2000US-191637P 11-JUL-2000; 2000US-0614150 23-MAR-2001; 2001WO-US09231 27-SEP-2001. Venter JC, (PEKE ) PE CORP NY. WO200171042-A2 Adams M, Li PWD, Myers 띺;

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                    708 A; .523 C; 522 G; 625 T; 0 other;
                                                      DNA;
                                                                                                                                                                             67.7%; Score 17.6; 1
83.3%; Pred. No. 56;
tive '0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                      2902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                      ВÞ
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                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insecticide;
                                                                                                                                                                                                      2378;
                                                                                                                                                                                                                                                                                                                                                                                       The invention
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23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                             Drosophila; developmental
                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 41803.
                                                                                               27-SEP-2001.
                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                            pharmaceutical;
                                                                                                                                                                                                          gene; ds.
                                                                                                                                                                                                                        biology;
                                                                                                                                                                                                                    cell signalling; insecticide;
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WPI; 2001-656860/75. Venter JC, (PEKE ) PE CORP NY Adams M, Li PWD, Myers

New isolated nucleic acid genes from Drosophila and interactions detection reagent for detecting 1000 for elucidating cell signalling and c 0 or more cell-cell

Claim 1; SEQ ID NO 41803; 21pp + Sequence Listing; English.

capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins at ftp.wipo.int/pub/published\_pct\_sequences The invention relates to an isolated nucleic acid detection capable of detecting 1000 or more genes from Drosophila. The The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from sequences (ABL01840 (ABB57737-ABB72072) ion reagent
. The invention i WIPO 19

Sequence 2902 BP; 695 A; 706 C; 690 G; 811 T; 0 other;

Ď. Matches Query Match Best Local 1169 L Similarity 20; Conserv GTCTTTCGCAGATCGGTACCTCAA 25 GTCCTTCGCCGGTCGCTACCTCAA 1146 Conservative 67.7%; 0 Score 17.6; Pred. No. 58; Mismatches DВ 23; . 4 Length Indels 2902; 0; Gaps

0;

RESULT 6 AAQ26928/ 6928/c AAQ26928 26-JAN-1993 (first entry) AAQ26928 standard; DNA; 3522 BP.

DNA encoding the novel toxin expressed by PS81A2.

Bacillus thuringiensis; lepidoptera; insect pest; insecticide;

Bacillus thuringiensis

CDS Location/Qualifiers
1..3522

18-JUN-1992.

AU9056291-A.

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Best Local
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 New isolated nucleic acid genes from Drosophila and
                                         WPI; 2001-656860/75
                                                                                                                         23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                 23-MAR-2001;
                                                                                                                                                                                               27-SEP-2001
                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 41815.
                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                              ABL30114;
                                                                                                                                                                                                                                                                                                                                                                                                        ABL30114 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3522 BP; 1171 A; 579 C; 766 G; 1006 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide toxin. With suitable nosts, the matter themselves, the sites of lepidopteran insects, e.g. to the insects, where they to the rhizosphere, philipplane or to a body of water, where they to the rhizosphere, by increased by the insects. The result is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microbial hosts, e.g. Pseudomonas, Azobacter, Erwinia, Serratia, Agrobacterium, Streptomyces species, etc. Expression of the tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The DNA sequence encodes a Bacillus thuringiensis endotoxin which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 29; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Controlling insect pests of lepidoptera family - contacting insects with suitable amt. of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-259364/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1990;
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                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                             pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be applied to the environment of target pests. retains the toxicity of the B.t. toxin. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           will proliferate and be ingested by the insects. The result is the control of unwanted insects. Alternatively, the microbe hosting the toxin gene can be treated under conditions that prolong the activity of the toxin produced in the cell. The treated cell can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene results in the intracellular prodn. and maintenance of
                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTTGGCCGATCAATACCTCAAT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in an expression system to transform a variety of
                                                                     Adams M,
                                                                                                                         2000US-191637P.
2000US-0614150.
                                                                                                                                                                 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            With suitable hosts, the microbes can be applied to
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                                                                     PWD,
detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.6;
Pred. No. 5
                                                                   Myers
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1000 or more and cell-cell
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RESULT 8
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL6175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 41815; 21pp + Sequence Listing; English
                                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                        WPI; 2001-656860/75
P-PSDB; ABB68327.
                                                                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in developmental
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                                                                                                                                                      interactions
                                                                                                                                                                genes from Drosophila
                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 31772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GTCTTTCGCAGATCGGTACCTCAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782 A; 963 C; 961 G; 998 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA;
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83.3%;
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                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4233
                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No. 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Drosophila. The invention elucidating cell signalling and otes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

is

Claim 1; SEQ ID NO 31772; 21pp + Sequence Listing; English

insecticides, therapeutics and pharmaceutical drugs. The discloses genomic DNA sequences (ABL16176-ABL30511), essequences (ABL01840-ABL16175) and the encoded proteins

for this patent did not form part of the printed

sequences (ABL0184) (ABB57737-ABB72072

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ABL13658/c
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Matches
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                                                                                                            Sequence 8173 BP;
                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                      The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                       useful in developmental biology and in elucidating cell signalling and insectionides, therapeutics in higher eukaryotes for the development of insections in higher eukaryotes for the development of discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                             New isolated nucleic acid
                                                                                                                                                                  (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                    genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                         Venter
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                             (PEKE )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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                                                                              Local
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                      204
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                                                                                                                                                                                                                                                                                                                                                2001-656860/75.
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                   JC, Adams M,
                 GTCTTCCCAAGGTCGGTACCTCAA 181
                                      GTCTTTCGCAGATCGGTACCTCAA 25
                                                                                                                                                                                                                                                                                                                                                                                            PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                           SEQ ID NO 35456; 21pp + Sequence Listing; English.
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2000US-0614150
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                                                                                                    2452 A; 1765 C; 1688 G; 2268 T;
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                                                                       Pred. No. 6
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                                                                                                                                                                                                                                                                                             elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 60;
0; Mismatches
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                   Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide SEQ ID NO 35456
                                                                                                                                                                                                                                                                                                                                                                  EW;
                                                                                  DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
                                                                                 23;
                                                           4.
                                                                                                                                    n part of the printed format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                          Indels
                                                                                                      0 other;
                                                                              Length 8173;
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                                                                                                                                                                                                                                                                                             and cell-cell
                                                         0;
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                                                        Gaps
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RESULT 11
                                                                                                                                                       В
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Matches Query Match Best Local (

Similarity

65.4%;

Score 17; Pred. No.

DB 23; 1.3e+02;

Conservative

0;

Mismatches:

0;

Gaps

specification, but was obtained in electroni
at ftp.wipo.int/pub/published\_pct\_sequences.

for this patent did not form

part of the printed format directly from

WIPO

The sequence data

ABB57737-ABB72072)

Sequence 7407 BP;

1810 A; 1780 C; 1770 G; 2047

T; 0 other Length 7407; Indels

Hyperthermophilic archaeon;

hyperthermophilic protein;

ds:

Pyrococcus abyssi genomic fragment #4

29-OCT-2001 AAH41225;

(first entry)

AAH41225 standard; DNA;

349980

ВP

313 CGTTTTTCGCATAGCTGTACCTTAA 289

CGTCTTTCGCAGATCGGTACCTCAA 25

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RESULT 10
ABL10262/c
ABL10262 standard;
useful in developmental biology and in elucidating cell signalling and inserticines; in higher eukaryotes for the development of inserticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG176-ABLIG511).
                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                        Claim 1; SEQ ID NO 25268; 21pp + Sequence Listing; English.
                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and interactions
                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
P-PSDB; ABB66159.
                                                                                                                                                                                                                                                                                                                                                     Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                          CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanogaster expressed
                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology;
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7407
                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pyrococcus abyssi.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                              inflammatory disease; I-8U; prostacyclin-stimulating factor; isf-2; tissue specific mRNA; insulin-like growth factor binding protein 6; OSF-1; gas-1; YMP; BTG2; pre-B cell stimulation factor benefits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence averlaps with the 3' end of AAH41224 and the 3' end of this sequence overlaps with the 5' end of AAH41226. The proteins of the present invention have various potential industrial uses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 349980 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                       cDNA of differentially expressed human gene osf-2.
                                                                                                                                                                                                                          25-SEP-2000
                                                                                                                                                                                                                                                                           AAA46670;
                                                                                                                                                                                                                                                                                                                         AAA46670 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-2000
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                                                                                                                        Differentially expressed human gene; cardiac disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: This patent is in the same patent family as WO200065062, contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            degrees centigrade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 since the proteins are stable at very high temperatures, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IFRE-) IFREMER INST FR RECH EX
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                            peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                     78251
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                    gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SD
eral benzodiazepine receptor; annexin II cellular ligand; p11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTCATCAGCGGATCGGCACCTCAA 78227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTCTTTCGCAGATCGGTACCTCAA 25
heart failure; dilated congestive cardiomyopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99FR-0005034.
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300001..349980
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AAH41226"
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                                                                                                                                                                                                                                                                                                                         CDNA;
                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99421 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%;
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                                                                                            man gene; cardiac disease; kidney
prostacyclin-stimulating factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76616 C; 77444 G;
                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eur D, Dietrich J,
Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96499 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 349980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                        disease;
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RESULT 13
AAQ48934
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                                                                                                                                                                                                          VQ.
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                      methods preventing, diagnosing and treating cardiac, kidney and inflammatory diseases associated with inappropriate expression of differentially expressed cardiac, kidney and inflammatory genes (e.g. AAA4668-79). These genes include I-8U, prostacyclin-stimulating factor, isf-2, tissue specific mRNA, insulin-like growth factor binding protein 6, OSF-1, gas-1, YMP, BTG2, pre-B cell stimulating factor homologue (SDF1a), peripheral benzodiazephne receptor, and cellular ligand of annexin II (pll), respectively. These diseases include congenital heart failure, dilated congestive cardiomyopathy, benefits the cardiomyopathy and the congestive cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypertrophic cardiomyopathy; restrictive cardiomyopathy; mitral valve disease; aortic valve disease; tricuspid valve angina pectoris; myocardial infarction; cardiac arrhythmia; pulmonary hypertension; arterial hypertension; renovascular arteriosclerosis; atherosclerosis; cardiac tumour; ss.
                                                                                                                                                                                                                                                                                                                                   hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary hypertension, arterial hypertension, renovascular hypertension, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA46668-79 represent differentially expressed human with disease states and disorders. The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preventing, diag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                          AAQ48934;
                                                                                                                                                                                                                                                                                             Sequence 3077
                                                                                                                                                                                                                                                                                                                        atherosclerosis and/or cardiac tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanton LW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200035473-A2
                                                                                                                  AAQ48934 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCIO-) SCIOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-451904/39
)B; AAY93596.
                                                                                                                                                                                      715
                                                                                                                                                                                                                                          l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     states such as
                                                                                                                                                                                                       CTTTCGCAGATCGGTACCTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosing and treating cardiac, kidney and inflammatory sing cardiac genes, that are differentially expressed in tes such as cardiac arrhythmia and arteriosclerosis
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White RT,
                                                                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0113008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US29941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 28..2367
                                                                                                                                                                                                                                                                                               1032 A;
                                                                                                                  cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170pp; English
                                                                                                                                                                                                                                                      63.8%;
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                                                                                                                                                                                                                                                                                               571 C;
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Pred. No. 1
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                                                                                                                   3092
                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                               632 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewicki JA,
                                                                                                                 BP.
                                                                                                                                                                                                                                                                                               842 T; 0
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                                                                                                                                                                                                                                                                     BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GF;
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Bone-related protein; bone; diagnosis; disease; greell adhesion; guiding; induction; metabolic bone

growth factor;

hOSF-2pl. 15-APR-1994

(first

entry;

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Homo

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Best Local
        14-MAR-2002.
                                                                         CDS
                            WO200220055-A1.
                                                                                                                                                         DNA encoding OSF-2 protein associated protein #3.
                                                                                                           Homo sapiens.
                                                                                                                             human; gene;
                                                                                                                               Heart failure; OSF-2 protein; gene therapy; transgenic animal;
                                                                                                                                                                                                              ABK49493
                                                                                                                                                                                      15-JUL-2002
                                                                                                                                                                                                                                 ABK49493
                                                                                                                                                                                                                                                                                                                                                                                               OSF-2 plays an important role in the formation of bone, by acting a growth factor or adhesion or "guiding" protein to attract cells to the site of bone induction. In a pharmaceutical compsn. it can be applied in metabolic bone diseases.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian OSF-2 protein - obtd. from diagnosis and treatment of metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-304910/39.
P-PSDB; AAR41868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tezuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens (placenta).
                                                                                                                                                                                                                                                                                                                                       Similarity
19; Conserv
                                                                                                                                                                                                                                 standard; DNA; 3092
                                                                                                                                                                                                                                                                                      CTTACACAAATTGGTACCTCAAT 747
                                                                                                                                                                                                                                                                                                           CTTTCGCAGATCGGTACCTCAAT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 14-18; 58pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOECHST JAPAN LTD.
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                                                                                                                                                                                   (first entry)
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                                                                                ocation/Qualifiers
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38..101
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                                                                                                                                                                                                                                                                                                                                             63.8%; Score 16.6;
82.6%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                             associated protein #3"
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bone disease
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Matches
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                          P-PSDB; AAR74302
                                     WPI; 1995-178826/23.
                                                                    Bao S,
                                                                                                                               29-OCT-1993;
                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                             31-OCT-1994;
                                                                                                                                                                                            04-MAY-1995.
                                                                                               (DAND ) DANA FARBER CANCER INST
                                                                                                                                                                                                                        W09511923-A.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                Tumour marker;
                                                                                                                                                                                                                                                                                                                                                                            TCI gene
                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ90112 standard; cDNA; 3126 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3092 BP; 1035 A; 573 C; 638 G; 846 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ90112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes preventives or remedies for heart failure comprising a substance inhibiting the expression of an OSF (undefined)-2 protein or function of the protein or function of a target molecule of the OSF-2 protein. The remedies are for heart failure, and are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remedies for heart failure obtained by inhibiting expression of OSF-2 gene or protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provide treatment and help adjust OSF-2 associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 61-66; 80pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-371858/40.
P-PSDB; AAU79825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           applicable for gene therapy. Diagnosis can also be achieved by monitoring gene expression and protein production. Transgenic animals are useful for studying the degree of disease deterioration and onset risk forecast to provide treatment and help adjust lifestyle. This sequence encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000JP-0273644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001; 2001WO-JP07787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                   'Chen LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                              9305-0146488
                                                                                                                                                           94WO-US12502
                                                                                                                                                                                                                                                                                                                                            invasive;
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                                                                                                                                                                                                                                                  Location/Qualifiers
43..2376
/*tag= a
                                                                   Liu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.8%;
                                                                                                                                                                                                                                                                                                                                            metastatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.6; DB 24
Pred. No. 1.8e+02;
                                                                                               INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
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0

New tumour marker TC1,

corresp. DNA and monoclonal antibody - for

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Query Match 63.8%;
Best Local Similarity 82.6%;
Matches 19; Conservative (
                                                                                                                                                                                                                 The sequence is that of the TCI gene which encodes the TCI tumour marker protein. The gene and its product may be used to detect tumours in blood, urine or sputum. Inhibitors of TCI are used to treat late stage cancers and for preventing tumour cell metastasis. See also AAQ90113-25.
                                                                                                                                          Sequence 3126 BP; 1035 A; 611 C; 656 G; 824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting, preventing and treating tumours, esp. in breast, colon and gastrointestinal tract cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 84pp; English.
Score 16.6; DB 16; Length 3126;
Pred. No. 1.8e+02;
0; Mismatches 4; Indels 0;
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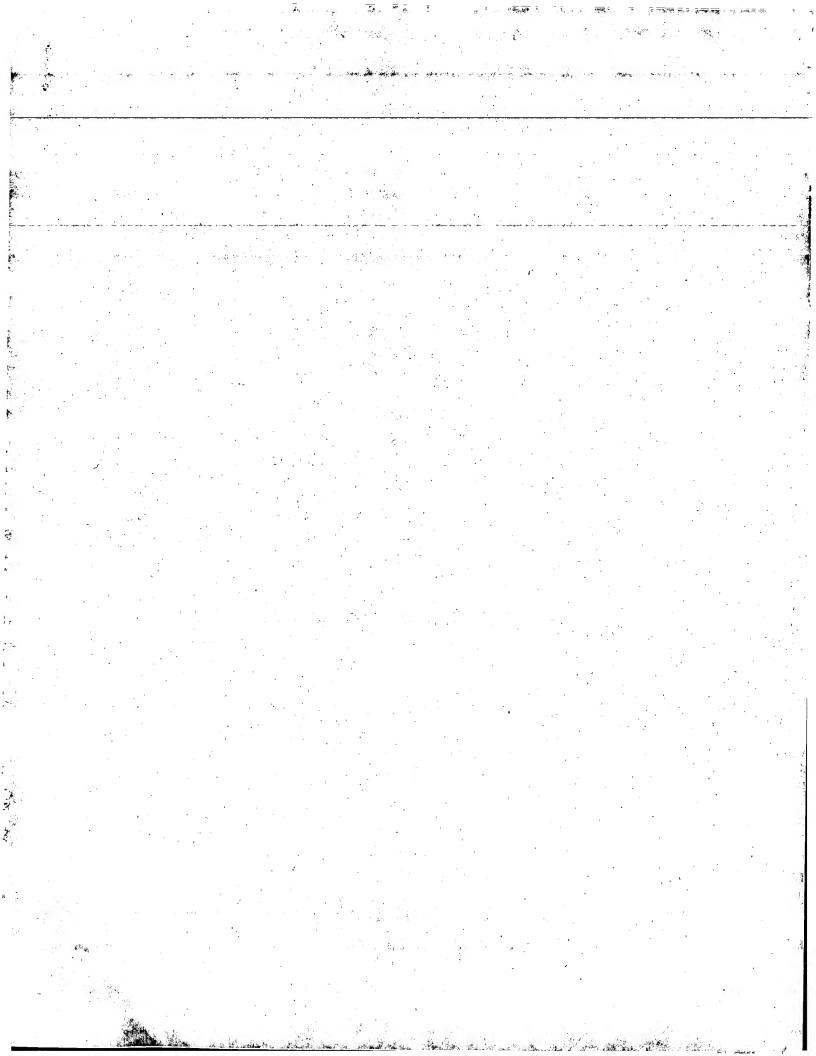
4; Indels

0; Gaps

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Search completed: July 10, 2003, 19:52:45 Job time: 57.8629 secs



OM nucleic - nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 July 10, 2003, 18:15:28; Search time 11.627 Seconds (without alignments) 685.785 Million cell updates/sec
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26
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Issued_Patents_NA:*
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                                5164180-3
US-08-257-999-1
US-08-478-507-6
US-09-128-275A-6
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US-09-253-427-6
US-09-251-0178-187
US-09-502-653-7
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US-09-018-211-1
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US-08-961-527-172
US-08-975-762-45
US-09-295-028-45
US-09-106-582-45
US-09-255-829-28
US-08-040-751-4
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 Sequence 3, Appli	Sequence 18, Appl	6,	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 18, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 18, Appl	•	Sequence 18, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 465, App	

			STRANDEDNESS: double TOPOLOGY: circular
			. H
			TELEX: 706141 INFORMATION FOR SEQ ID NO: 1098:
			TELEFAX: 650-494-0792
			TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
			NUMBE
		•	REGISTRATION NUMBER: 32.430
			Y/AGENT I
			APPLICATION NUMBER: PCT/AU98/01023
			FILING DATE: 09-APR-1998
			Α.
			APPLICATION DATA: PP1546
			ING DATE: 31-DEC-
			APPLICATION DATA: PP1182
			CLASSIFICATION:
			FILING DATE: 23-DEC-1998
			- ≥
			FastSEQ
			OPERATING SYSTEM: Windows
			PE
			ZIP: 94304-1018
			STATE: CA
			Palo Alto
			ADDRESSEE: MORRISON & FOERSTER
			PONDENCE ADDRESS:
THEREO	USES	AND	ES: 1.1
			GENERAL INFORMATION: APPLICANT: Ross, Bruce C.
			Neguence 1030, Apparention 03/0322101/0
٠			09-221-017B-1098

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JS-09-221-017B-1098
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-477-396A-1
                                                                                                                                      TELEFAX: (617) 451-0313
NFORMATION FOR SEQ ID NO:
                                     ANTI-SENSE:
                          FEATURE:
                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                              REFERENCE/DOCKET NUMBER: | DETELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No. 587
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1...495
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                                                                                   ANDEDNESS:
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                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CGACTGTCACGGATCGGTACTTCAA 252
                                                                                                                                                                                                                        DATE: 31-OCT-1994
/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                          ARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                  ATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ONDENCE ADDRESS:
                                                                                                                                                                                                                                                            ATION NUMBER: US 08/448,388
DATE: 28-MAY-1996
PLICATION DATA:
                                                                                                                                                                                             Heine, Holliday C.
Heine, Holliday C.
Heine, Holliday C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTCTTTCGCAGATCGGTACCTCAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08477396A
                                                                                                           636 base pairs
          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
 1..636
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                                                                                                                                                                                                                                                                                                               US 08/146,488
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Pred. No.
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LOCATION:
US-08-426-627-3
Query Match
Best Local Similarity
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Best Local S
                                                                     FEATURE:
NAME/KEY:
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                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: JP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                               LOCATION: · join(38..2375)
                                                                                                                     NAME/KEY:
                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 35,178
REFERENCE/DOCKET NUMBER: 02481-1285-00000
                                                                                                                                                                                                                                                                                                                                             NAME: Hammond, Alan W
REGISTRATION NUMBER:
                                                                                                                                            ISSUE TYPE:
                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                       OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION:
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                                                                                                                                                                                                                               nucleic acid
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19; Conserv
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                                                                                                                                                          Homo sapiens
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                                                      mat_peptide
join(101..2375)
                                                                                                                                                                                                    linear
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                                                                                                                                            Placenta
                                                                                                                                                                                      cDNA to mRNA
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27-MAR-1992
                                                                                                                                                                                                                   double
63.8%;
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Pred. No. 29;
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Pred. No. 23
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            DB 1;
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          Length 3092;
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8-477-396A-3

Matches

19; Conservative

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Mismatches

Indels

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Gaps

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US-08-426-627-5

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LOCATION:
US-08-477-396A-3
                                                                                                   Matches
                                                                                                                 Query Match
Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 3126 hard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION DATA:
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                                                                                                                                                                                                                             YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                               TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                           ECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILING DATE: 28-MAY-1996
OR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER: US 08/146,488
                                                                                                                                                                                                                                                                       RANDEDNESS:
                                                                                                                                                                                                                                                            OLOGY:
                                               748
                                                                        4 CTTTCGCAGATCGGTACCTCAAT 26
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                                               CTTACACAAATTGGTACCTCAAT 770
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43..2376
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Liu, Yuan
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31-OCT-1994
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                                                                                                  0; Mismatches
                                                                                                                 Score 16.6;
Pred. No. 29;
                                                                                                                              DB 2;
                                                                                                                            Length 3126;
                                                                                                   Indels
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                                            RESULT 6
US-08-772-440-33
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Sequence 33, Application US/08772440 Patent.No. 6046158 GENERAL INFORMATION:
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RESULT 5

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US-08-426-627-5
                                                                     Best Local Similarity
                                                                                 Query Match
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                                                                                                                                                              FEATURE
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                        CELL TYPE:
                                                                                                                                                                             LOCATION:
                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 4-71501 FILING DATE: 27-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0
FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                 ECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                  POLOGY:
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719 CTTACACAAATTGGTACCTCAAT 741
                                                        19;
                             4 CTTTCGCAGATCGGTACCTCAAT 26
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                                                        Conservative
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join(97..2540)
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                                                                                                                                                                                                                                    Homo sapiens
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                                                                     63.8%;
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                                                                     Score 16.6;
Pred. No. 29;
                                                        Mismatches
                                                                                    DB 1;
                                                                                    Length 3253;
                                                       Indels
                                                       0;
                                                       Gaps
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US-08-772-440-33

OTHER INFORMATION: OTHER INFORMATION:

/mod\_base= OTHER
/note= "Y = C or T"

0;

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LOCATION:
                                                                              NAME/KEY:
                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 URBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                    IAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMATION FOR SEQ ID NO:
QUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                       KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /KEY:
                                                                                                                                                                INFORMATION: /mod_base=INFORMATION: /note= "R =
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                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arker, David L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10409 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.O. Box 4433
                                                              modified_base 3457..9998
modified_base
3595..9999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                              modified_base 3405..6871
                                                                                                                                                                                            modified_base 3479..6422
                                                                                                                                                                                                                                                                                                                                                                                     modified_base
3406..6470
                                                                                                                                                                                                                                                           modified_base 3497..3607
                                                                                                                                                                                                                                                                                                                                   modified_base
                                                                                                                                                                                                                                                                                                                         3564..7896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified_base
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                                    /note
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                                                                                                 /mod_base= OTHER
/note= "S = C or
                                                                                                                                                                                                                                /mod_base= OTHER
/note= "N = A or C
                                                                                                                                                                                                                                                                                                                                                           /mod_base-
/note= "K =
                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "D = A or G
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/note= "M = A or
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                                                _base= OTHER
                                   "W = A or T"
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DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
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590 CGGCTTACGCAGAGCGCTTGCTCAAT 615

RESULT 8 US-09-018-211-1

Sequence 1, Patent No. (

APPLICANT: Lawlor, TITLE OF INVENTION:

Elizabeth

No: 6048716el Compounds

INFORMATION:

Application US/09018211

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US-08-844-086-1
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                                                     Query Match
                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence I
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607993.4
FILING DATE: 18-APR-1996
                                                                                                                                                                                                       TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                           OMPUTER READABLE FORM
                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER OF SEQUENCES:
                                                                                                                 STRANDEDNESS:
                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 18-APR-1997
                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       OUNTRY: USA
IP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2852 TCTTTGGCAGNTGAGTTCCTCAAT 2875
                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, Application US/08844086
5. 5866390
1 CGTCTTTCGCAGATCGGTACCTCAAT 26
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TCTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA
                                                                                                                         2502 base pairs ucleic acid
                          Conservative
                                                                                                                                                                                            610-270-5090
                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                       Linear
                                                                                                                                                                                                                                                                                                                                                                                                    IBM
                                                                                      Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                Compatible
                                     63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elizabeth
No. 5866390el Compounds
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                                                                                                                                                                                                                                        38,891
                                                                                                                                                                                                                                P31457-4
                                     Score 16.4;
Pred. No. 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.6;
Pred. No. 34;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                 DВ
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                                                 Length 2502;
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                        0
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                     Gaps
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NUMBER OF SEQUENCES:

STREET: 709 Swedeland CITY: King of Prussia

2: SmithKline Beecham Corporation 709 Swedeland Road

ADDRESSEE:

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Matches
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                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         quence 172, Application US/08961527 tent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 18-APR-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                             PPLICANT:
                                                                   OPERATING SYSTEM: MSI
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                              TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: .USA
ZIP: 19406-0939
                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                      APPLICATION NUMBER:
                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                DDRESSEE:
                                                                                                                                                                        ITY: Rockville
TATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSIFICATION: 435
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APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                              1 CGTCTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                            20850
                                                                                                                                                                                                                                                                                                                                                                                              CGGCTTACGCAGAGCGCTTGCTCAAT 615
                                                                                                                                                                                                    9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2502 base pairs
                                                                                                                                                         USA
                                                                                                                                                                                                                                                                           Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                          HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 2.0
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                                                                                                              Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                 MSDOS version 6.2
                                                                                                                                                                                                                 Genome Sciences,
                                                                                                                                                                                                                                                           Streptococcus pneumoniae Polynucleotides and Sequences
                                                                                                                                                                                                                                                 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9607993.4
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                                       US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۳.
                                                                                                              3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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Matches
           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/08975762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                        TELEFAX: 206-682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 11770 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                       MOLECULE TYPE:
                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local 20;
                                                                                                                                                                                              NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION
                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                       FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                           LENGTH:
                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.818 CGGCTTACGCAGAGCGCTTGCTCAAT 7843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Seattle
                                                                                         2373 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                   Washington
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTCTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                            6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                       206-682-603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton, Raymond
JENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                 PatentIn
                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEED and BERRY LLP
                                                     DNA (genomic)
                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.1%;
61.5%; Score 16; 79.2%; Pred. No.
                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                    US/08/975,762
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             Length 2373;
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RESULT 12 | US-09-106-582-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                    NFORMATION FOR SEQ ID NO: 45:
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                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Ehrlichia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/O
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
                                                                                              TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
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ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G
                                                                                                                           REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 29-JU
                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                      CLASSIFICATION:
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E INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
OF SEQUENCES: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6306402
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                                    2373 base pairs
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                                                                                   206-682-6031
                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                  29-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 16; DB 79.2%; Pred. No. 55; tive 0; Mismatches
                                                                                                                                                                                                           US/09/106,582
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                                              Matches
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                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                               NAME/KEY:
LOCATION:
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                             Local Similarity es 19; Conserv
                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                              NAME: ESMOND, ROBERT W
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/782,893 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/GB97/02273 FILING DATE: 22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
2 GTCTTTCGCAGATCGGTACCTCAA 25
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                                                                                                                                                                                                             2574 base pairs
                                           Conservative
                                                                                                                                                                                                                                                         202-371-2540
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Foster, Keith Alan
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79.2%;
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                                                                                                                                                                                                                                                                                                              32,893
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                                     Score 16; DB Pred. No. 56; 0; Mismatches
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                                                                  DB 4;
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                                                                Length. 2574;
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1570 GTTTTTCGTAGACCGGGACGTCAA 1547

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Application US/08040751

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Matches 19
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Patent No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: Lambo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                          PPLICANT:
                                                                                             PPLICANT:
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                              DRRESPONDENCE ADDRESS
                                                              THE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: aizawai
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SALIWANCHIK, DAVID R. REFERENCE/DOCKET NUMBER: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1
CLASSIFICATION:
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FILING DATE: 19930329
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                                                                                                                                                                                                                               252 TCTTTGGCCGATCAATAGCTCAAT 229
                                                                                                                                                                                                                                                                                              l Similarity
19; Conser
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                                                                                                                                                     Application US/08291368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3522 base pairs
: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                        Sick, August J. VENTION: No. 5686069el Bacillus thuringiensis Isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                     Lambdagem - 11 (tm) Library of August Sick
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N: No. 5407825el Bacillus thuringiensis isolates
N: active against Lepidopteran Pests and Genes E
N: Lepidopteran-active Toxins
                                                                                                          Jewel M.
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                                                           Active Against Lepidopteran Pests
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                                                                                                                                                                                                                                                                                                         Score 16;
Pred. No.
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Search completed: July 10, 2003, 20:27:41 Job time: 13.627 secs

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Matches
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LIBRARY: Lambd
CLONE: 81A2
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                 OLECULE TYPE:
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                                                                       Local
                                                                                                                                                                               STRAIN: aizawai
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07 FILING DATE: 15-OCT-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: . 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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252 TCTTTGGCCGATCAATAGCTCAAT 229
                 3 TCTTTCGCAGATCGGTACCTCAAT 26
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                                                                        Similarity
                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                       Conservative
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                                                                                                                                                                                                           Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                   double
                                                                     61.5%;
79.2%;
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                                                                       Score 16;
Pred. No.
                                                         Mismatches
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                                                                                     Length 3522;
                                                         Indels
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 length: 0
length: 2000000000
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Published_Applications_
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                                                          US-10-217-371-3

US-10-217-371-9

US-10-217-371:11

US-10-217-371-1

US-10-217-371-1

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US-10-087-631B-1
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576.891 Million cell updates/sec
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53770, A
4795, Ap
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                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 26
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10087631B Publication No. US20030054372A1 GENERAL INFORMATION:
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2002-0
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A TITLE OF INVENTION: CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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2002-03-01

US/10/087,631B

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60.8	60.8	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	63.1	63.1	63.1	63.1	63.8	63.8
333	135	7195	4417	4416	4235	3969	3120	3120	2373	2373	2184	1794	1410	945	705	614	490	168	25	5289	5289	1794	617	9025608	397658
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US-09-294-093B-124	US-09-878-574-7595	US-09-851-410-6	US-10-128-714-5395	US-10-128-714-395	US-10-198-846-10905	US-10-177-293-386	US-10-128-714-5261	US-10-128-714-261	US-09-798-042-45	US-09-159-469-45	US-09-801-368-295	US-09-822-846-139	US-09-938-842A-818	US-10-084-546-5	US-09-815-242-7385	US-09-770-149-838	US-09-918-995-33372	US-09-878-574-13775	US-10-215-112-6258	US-10-128-714-5179	US-10-128-714-179	US-09-815-242-9128	US-09-770-149-820	US-10-156-761-1	US-09-813-320-3
Sequence 124, App	Sequence 7595, Ap	Sequence 6, Appli	Sequence 5395, Ap	Sequence 395, App	Sequence 10905, A	Sequence 386, App	Ξ	Sequence 261, App	Sequence 45, Appl	Sequence 45, Appl	Sequence 295, App	Sequence 139, App	Sequence 818, App	Sequence 5, Appli	Sequence 7385, Ap	Sequence 838, App	Sequence 33372, A	Sequence 13775, A	Sequence 6258, Ap		Sequence 179, App	Sequence 9128, Ap	Sequence 820, App	Sequence 1, Appli	Sequence 3, Appli

#### ALIGNMENTS

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RESULT 2
US-10-087-631B-12
                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: complement to ST280 US-10-087-631B-8
                                                                                       Sequence 12, Application No. US20 GENERAL INFORMATION:
TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING TITLE OF INVENTION: CONTROL FILE REFERENCE: 1803-335-999 CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
                                                                          APPLICANT: JAEGER,
                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                             Similarity
                                                                                                        Application US/10087631B
No. US20030054372A1
                                                                                                                                                                                                                                                       Conservative
                                                                          STEPHAN
                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                        Score 26;
Pred. No.
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                        0.0014;
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                                                                                                                                                                                                                                                                                   Length 26;
                                                                                                                                                                                                                                                          Indels
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ORGANISM: Artificial Sequence; PEATURE:
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence; QS (pc) HCV being parallel;
OTHER INFORMATION: complement to according region of HCV type I genome
US-10-087-631B-11
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-087-631B-11
                                                                                                                        SEQ ID NO 53770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: //
OTHER INFORMATION: using the primers ST280pc and ST778pc
US-10-087-631B-12
                                                      ORGANISM: Homo sapien
-10-098-263B-53770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                         TYPE: DNA
                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60, PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/098,263B
                                                                                                                                        SOFTWARE:
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                                                                                                                                                    WIMBER OF SEQ ID NOS:
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Best Local
                                                                         ORGANISM:
                                                                                                                                                                                                                                        NPPLICANT: MITTMAN, MICHAEL TITLE OF INVENTION: Human MITTLE REFERENCE: 3118.1
                                                                                                                                                                                                                                                                                                 quence 53770, Application US/10098263B blication No. US20030104410A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                      0-098-263B-53770/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/087,631B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A LILE REFERENCE: 1803-335-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn version 3
                                                                                                                                                                                                                                                                                                                                                                                              CGTCTTTCGCAGATCGGTACCGCAAT 82
                                                                                                                          lcroarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10087631B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US20030054372A1
                                                                                                                                                                    2001-03-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEPHAN
                                                                                                                                                                                                                                                  Human Microarray
65.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 24.4; DB 9; Length 943; 96.2%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-03-01
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96.2%;
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Score
Pred.
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Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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DB 9;
46;
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            Length 25;
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RESULT 6
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                                                                   US-10-040-862-4795
                                     Sequence 4795, Application US/10040862 Publication No. US20030078396A1
                           GENERAL INFORMATION:
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            APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URRENT APPLICATION NUMBER: US/09/796,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                               NO 4795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/186,126
                                                                                                                 438 CTTACACAAATTGGTACCTCAAT 460
                                                                                                                                          4 CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                            Similarity
19; Conserv
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Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATION NUMBER: 60/200,303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09796692
. US20020198362A1
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                                                                                                                                                                                   63.8%;
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                                                                                                                                                                                   Score 16.6;
Pred. No. 94;
                                                                                                                                                                      Mismatches
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INVENTION: Compositions a INVENTION: Hematological

gnancies

for the Detection,

Diagnosis and Ther

Retter, Marc Corixa Corporation

Mannion,

IOR APPLICATION NUMBER: US 60/186,126 IOR FILING DATE: 2000-03-01

REFERENCE: 014058-013520US

APPLICATION NUMBER: US/10/040,862 FILING DATE: 2001-11-06

R APPLICATION NUMBER: US 60/190,479 R FILING DATE: 2000-03-17

CATION NUMBER: US 60/200,545

2000-04-27

APPLICATION NUMBER: US 60/200,303

PLICATION NUMBER: US 60/200,779

2000-04-28 000-04-28

NUMBER: US 60/200,999

APPLICATION NUMBER: US 60/202,084

2000-05-04

2000-05-01

Best Local Similarity 82.6%; Matches 19; Conservative

0

Pred. No. 1.1e+02; 0; Mismatches 4

Indels

0; Gaps

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4 CTTTCGCAGATCGGTACCTCAAT 26

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                                 ; NAME/KEY: CDS
; LOCATION: (1)...(2190)
US-10-217-371-5
Query Match
                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10217371 Publication No. US20030073137A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                           CURRENT
                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/312,123 PRIOR FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                               10-217-371-5
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       PPLICANT: Sasaki, Hidefumi
PPLICANT: Auclair, Daniel
ITLE OF INVENTION: PERIOSTIN-BASED DIAGNOSTIC ASSAYS
ILE REFERENCE: 00530-099001
                                                                                   FEATURE:
                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 CTTACACAAATTGGTACCTCAAT 460
                                                                                                                                    2190
                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/217,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                              Dai, Meiru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                         2002-08-
 63.8%;
 Score 16.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
 DB 9;
Length 2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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; LOCATION: (1)...(2250)
US-10-217-371-13
                                                              NAME/KEY: CDS: LOCATION: (1)...(2253)
US-10-217-371-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-217-371-13
                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2253
Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10217371 Publication No. US20030073137A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2002-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-08-13 PRIOR APPLICATION NUMBER: US 60/312,123 PRIOR FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/217,371
CURRENT FILING DATE: 2002-08-13
                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sasaki, Hidefumi
APPLICANT: Auclair, Daniel
TITLE OF INVENTION: PERIOSTIN-BASED DIAGNOSTIC ASSAYS
FILE REFERENCE: 00530-099001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Lan Bo
APPLICANT: Dai, Meiru
                                                                                                                                                                                                                                                                                      APPLICANT: Sasaki, Hidefumi
APPLICANT: Auclair, Daniel
TITLE OF INVENTION: PERIOSTIN-BASED DIAGNOSTIC ASSAYS
FILE REFERENCE: 00530-099001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Chen, PPLICANT: Dai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         625 CTTACACAAATTGGTACCTCAAT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625 CTTACACAAATTGGTACCTCAAT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 82.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10217371
D. US20030073137A1
                                                                                                                                                                                                                                                                                                                                                     Dai, Meiru
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lan Bo
                                                                                                                                                                                                                                                                                                                                                                  Lan Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.8%;
                63.8%;
                                                                                                                                                                                                                                                                    US/10/217,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.6; D
Pred. No. 1.1e
0; Mismatches
   0
                Score 16.6;
Pred. No. 1
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1e+02;
                  .1e+02
                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
                               Length 2253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2250;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
   0
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   Gaps
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0,

; ORGANISM: Homo sapiens US-10-040-862-4795

Local

Similarity

63.8%;

Score 16.6; Pred. No. 94;

DB 9; Length 507;

SOFTWARE: FASTSEQ SEQ ID NO 4795 LENGTH: 507

CATION NUMBER: US 09/796,692

ID NOS:

for Windows Version 3.0

ATION NUMBER: US 60/223,378

-08-07

NUMBER: US 60/223,416

2000-08-03

us 60/222,903

NUMBER: US 60/218,950

-05-22

US 60/206,201

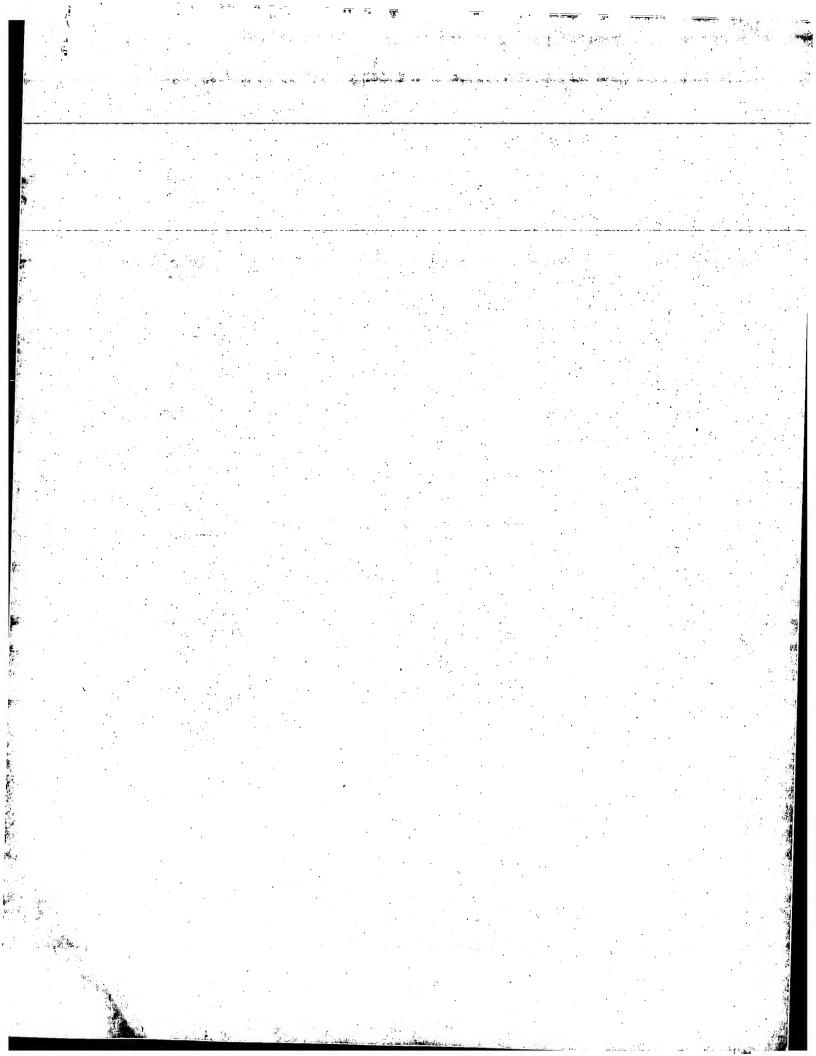
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Db
                                   Qy
                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)...(2313)
US-10-217-371-11
                                                                  Matches
                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10217371
Publication No. US20030073137A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sasaki, Hidefumi,
APPLICANT: Auclair, Daniel:
TITLE OF INVENTION: PERIOSTIN-BASED DIAGNOSTIC ASSAYS
FILE REFERENCE: 00530-099001;
CHERENT SANIEST STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                             ENERAL INFORMATION:
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                ORGANISM; Homo sapiens
                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1)...(2274)
10-217-371-9
                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICANT: Sasaki, Hidefumi
ICANT: Auclair, Daniel
E OF INVENTION: PERIOSTIN-BASED DIAGNOSTIC ASSAYS
REFERENCE: 00530-099001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/312,123 FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9, Application US/10217371
ion No. US20030073137A1
                                                                                                                                                                                                                     2313 .
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 CTTACACAAATTGGTACCTCAAT 710
CTTACACAAATTGGTACCTCAAT 710
                                                                                                                                                                                                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/217,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CTTTCGCAGATCGGTACCTCAAT 26
                            CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                   CATION NUMBER: US 60/312, 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTACACAAATTGGTACCTCAAT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                                                                              Dai, Meiru
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dai, Meiru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lan Bo
                                                                       63.8%; Score 16.6; 82.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-08-
                                                                                                                                                                                                                                                                                                                 US/10/217,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.6;
Pred. No. 1
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                          .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
.1e+02;
                                                                                    Length 2313;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2274;
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                                                      0;
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; NAME/KEY: CDS
; LOCATION: (1)...(2508)
US-10-217-371-1
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)
US-10-217-371-7
                                                                           Matches.
                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-217-371-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.8%;
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/217,371
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 60/312,123
PRIOR FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sasaki, Hidefumi
APPLICANT: Auclair, Daniel
TITLE OF INVENTION: PERIOSTIN-BASED DIAGNOSTIC ASSAYS
FILE REFERENCE: 00530-099001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10217371 Publication No. US20030073137A1
                                                                                                                                                                                                                                                                                                     UMBER OF SEQ ID NOS:
                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 23
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/217,371
                                                                                                                                                                                                                                                   ENGTH: 2508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIOR APPLICATION NUMBER: US 60/312,123 RIOR FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: Sasaki, Hidefumi
PPLICANT: Auclair, Daniel
ITLE OF INVENTION: PERTOSTIN-BASED DIAGNOSTIC ASSAYS
ILE REFERENCE: 00530-099001
688 CTTACACAAATTGGTACCTCAAT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            688 CTTACACAAATTGGTACCTCAAT 710
                     4 CTTTCGCAGATCGGTACCTCAAT 26
                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10217371
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dai, Meiru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1)...(2337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dai, Meiru
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US20030073137A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US20030073137A1
                                                                                      63.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-08-1
                                                                   Score 16.6; DB 9;
Pred. No. 1.1e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.6;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG
                                                                                                 Length 2508;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2337;
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                                                              Gaps
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RESULT 14

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; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSEQ for Win
; SEQ ID NO 179
; LENGTH: 3077
; TYPE: DNA,
; ORGANIZM: Homo sapiens
US-10-171-311-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-176-847-45
Sequence 45, Application US/10176847
Publication No. US20030068636A1
GENERAL INFORMATION:
APPLICANT: Veiby, Petter Ole
Search completed: July 11, 2003, 15:02:06 Job time: 80.164 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-176-847-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity barrances
19; Conservative
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 2937
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/176,847
CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/335,936 PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equence 179, Application US/10171311 ublication No. US20030087270a1
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: MRI-039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR ITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTILE OF INVENTION: AND OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLICANT: HOETSH, Sebastian
TILE OF INVENTION: NOVEL GENES, COMPOSITIONS,
TILE OF INVENTION: IDENTIFICATION, ASSESSMEN
OF CERVICAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRENT APPLICATION NUMBER: US/10/171,311
RRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715 CTTACACAAATTGGTACCTCAAT 737
                                                                                            4 CTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                               19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen, Yan
Zhao, Xumei
Monahan, John
Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glatt, Karen
Gannavarapu, Manjula
                                                                                                                                                                                                                                                                                                                    for Windows Version 4.0
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                                                                                                                                                                 63.8%;
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                                                                                                                                                                 Score 16.6;
Pred. No. 1
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Pred. No. 1.
                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITIONS, KITS, AND METHODS FOR ASSESSMENT, PREVENTION, AND THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1e+02;
                                                                                                                                                                   .1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2937;
                                                                                                                                                                                Length 3077;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                 0
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                                                                                                                                             Gaps
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AA53

AC087346 HS\_2191\_B BF588219 FM1\_30\_BO AC255220 mgxb0009D BF757321 MR0-CT045 BI172474 RE14977.5 AV524463 AV524463 AA538976 LD18659.5

BM870563 mgns010xH AZ147865 SP\_0014\_A B1164958 RE04739.5 B1171702 RE13532.5 BH177119 008\_F 21-AL614077 T3 end of B1227641 RE24745.5 B11770103 RE11457.5 B1362843 RE47517.5 B1362843 RE47517.5 B1362843 RE47517.5 AA263759 LD07041.5 AV517896 AV517896 B1213740 RE19230.5 B1165983 RE09924.5 H16552 yml3d12.s1

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Title: Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 08
Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16154066 seqs, 8097743376 residues
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                    em_estba:
                             em_gss_inv:*
em_gss_pln:*
em_gss_vrt:*
em_gss_fun:*
em_gss_mam:*
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AA820697

AI515767 LD41430.5 AI999483 701556093 BI169019 RE09972.5 BI171671 RE13491.5 BI356268 RE42371.5 AA820697 LD24550.5 BI483494 RE68829.5 BI230919 RE16187.5 BI138807 RE41867.5 BH175201 002\_B\_14

BI48549

BI238807 BH175201 CNS0718R BH655017

ALIGNMENTS

AQ900643  AQ900643  BE 3171_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=14 Row=A, DNA sequence. AQ900643  AQ900643.1 GI:6356833  GSS. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 961) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 9380589 Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Fax: (206) 616-3887 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
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Result

Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the

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Score

Query Match

Length DB

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SUMMARIES

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75.4 73.8 73.8 71.5 71.5 70.0

AL351632 BF098973

CNS02NJM

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COMMENT
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                                                                                                                                                                                                                                                                    Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
urther details.
                                         (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Mouse ESTs (Aizawa, K. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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Class: BAC ends
High quality sequence stop: 961.
                                                 High-efficiency full-length cDNA cloning. Methods Enzymol.
                                                                                    Automated filtration-based high-throughput plasmid preparation ystem. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                            rehalose and its application for the synthesis of full length DNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Omaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                          hermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                         aboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oshiki, A., Muramatsu, M. and Hayashizaki, Y.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                   ulu-1, r., Nishiyama, r., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Okazaki, r., Muramatsu, M. and Hayashizaki, r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kusakabe, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT Approved Human
/sex="male"
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ki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
                                                                                                                                                                                                                                                                                                                                                                   Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.5e+02;
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1, 12 days embryo spinal ganglion
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                                                 303,
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source

/organism="Lycopersicon /cultivar="TA496"

esculentum'

ocation/Qualifiers

. 698

/clone\_lib="tomato flower,
/tissue\_type="flower" /db\_xref="taxon:4081" /clone="cTOA23N9"

buds 0-3 mm\*

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JOURNAL COMMENT
FEATURES
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KEYWORDS
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Best Local S
Matches 21
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                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                           Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                     Clemson University
                                                                              100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                       Clemson University Genomics Institute
                                                                                                                                                Contact: CUGI
                                                                                                                                                                Unpublished
                                                                                                                                                                                 Generation of ESTs
                                                                                                                                                                                           van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fr. Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EST544445 tomato flower, clone cTOA23N9 5' end, mI
                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
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               primer: T3
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nilarity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was cleaved with BanHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

44 c 61 g 38 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcriptase and subsequently enriched for full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contributed to prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primed with a primer
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spinal ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage="12 days embryo"
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                                                                                                                                                                (2001)
                                                                                                                                                                                                                                                            to 698)
                                                                                                                                                                                                                                                                                                                                                                                                                                          698 bp mRNA linear EST 18-OC flower, buds 0-3 mm Lycopersicon esculentum end, mRNA sequence.
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0; Mismatches
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Pred. No. 1.7e+02;
                                                                                                                                                                            tomato flower tissue,
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qr05h12.xl Soares_total_fetus_Nb2HF8_9w Homo
IMAGE:1940039 3', mRNA sequence.
AI351632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 460)
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                             GTCTTTCGCAGATCGGTACCTCAAT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="0-3mm buds"
/note="Vector: pBluescript SK(-); Site_1: EcoRI;
XhoI; supplier: Cornell University; sequencing: Institute for Genomic Research; Flower buds and it
                                                                                                                                                         constructed
91 c
                                                                                                                                                                                                                                                                             /note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1940039"
                                                                                                                                                                                                                             (Pharmacia), digested with Not
                                                                                                                                                                                                                                                                                                                                                                      'dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="Soares_total_fetus_Nb2HF8_9w'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -40UP from Gibco
                                                                                                                                        Eco RI sites of the modified pT7T3 vector. Library t through one round of normalization, and was structed by Bento Soares and M. Fatima Bonaldo. "
91 c 107 g 131 t
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87.5%;
                                                                                   71.5%;
84.0%;
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                                                                                   Score 18.6; DB 9;
Pred. No. 3.7e+02;
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Pred. No. 2.2e+02;
0; Mismatches 3;
                                                                Mismatches
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RESULT 6
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Tetraodon nigroviridis genome survey sequence T7 end of c
151J19 of library G from Tetraodon nigroviridis, genomic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GTCTTTCGCAGATCGGTACCTCAAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM9170 row: e column: High quality sequence stop: 636. Location/Qualifiers
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                       1 (bases 1 to 182)
Rosst-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                        GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1029)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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295 c 300 g 177 t
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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="FVB/N"
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Pred. No. 4.4e+02;
0; Mismatches 4;
provided by genome wide analysis using
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                                                                                                                                                                URL:http://genome-res@gsc:riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshki, A. Muramete, K., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka,Y., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Muramete, M., Tanaka, T., Yasunishi,A., Yoshida,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Hanmalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Losses 1 to 234)

(bases rninci,P., Nishiyama,Y., Westöver,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Mouse ESTs (Alzawa, K. et al. 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB593576 RIKEN full-length enriched, 4 days neonate male Mus musculus cDNA clone B430103F24 5', mRNA sequence.
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Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nouse mouse
                                                                                                                                                                                                                                                                                                                          7-22 Suehiro-cho,
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26 c 55 g 39 t 4 others
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/db_xref="taxon:99883"
/clone="151J19"
/clone=11b="G"
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lt,A., Quetier,F.,
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Pred. No. 4.7e+02;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                          Yokohama, Kanagawa
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Bernot,A. and
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Yoshiki,A., Muramatsu,M.

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SOURCE
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BB600933/c
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Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hizozane, T., Hodoyama, Y., Imotani, K., Ishil, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Rakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, X., Shibata, Y., Shinayawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,
                                                                                                                                                                                                                                                                                                       musculus
BB600933
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                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 242)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system. Genome Res. 9 (5), 463 470 (1999)
Carningi, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                           RIKEN full-length enriched, 13 days embr
cDNA clone D430002D01 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN. Division of Experimental Animal Research in Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: Sall; Site_2: BamHI; cDNA library was
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/lab_host="DH10B"
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Pred. No. 5e+02;
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Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
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ORGANISM
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                                                                                                        BB569672 RIKEN full-length enriched, 13 cDNA clone 3930401E03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                  4 CTTTCGCAGATCGGTACCTCAAT 26
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Contact: Yoshihide Hayashizaki
                                                                BB569672.1 GI:11460580
Mus musculus
                                                                                                                                                        BB569672
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                   house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -22 Suehiro-cho, Tsurumi-ku,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pBluescript KS(+) after bulk excision from Lambda FLC I." 44 \text{ c} 88 g 50 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer adapter of sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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/clone="D430002D01"
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/_stage="13 days embryo"
b_host="DH10B"
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87.0%;
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Query Match Best Local Matches

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Score 18.2; DB Pred. No. 5e+02;

DB 10;

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AUTHORS
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BASE COUNT
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Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y.,
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Mammalia; 1
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URL:http://genome.gsc.riken.go.jp/
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omaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High-efficiency full-length cDNA cloning. Methods Enzymol. 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                             modified pBluescript KS(+) after bulk excision
                                                                                                            was cloned into the XhoI and BamHI sites.
                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                         prepared by using trehalose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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/strain="C57BL/6J"
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                                                                                                            Vector: a
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                                                                             from Lambda
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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290 bp mRNA linear EST 30:NOV-200
BB592646 RIKEN full-length enriched, adult male corpora
quadrigemina Mus musculus cDNA clone B230104022 5', mRNA sequence.
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High-efficiency full-length cDNA cloning.
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Irhermostabilization and thermoactivation of thermolabile enzymes by crehalose and its application for the synthesis of full length DNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Pomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-res@gsc.riken.go.jp,
tp://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                visit our web site (http://genome.rtc.riken.go.jp) for
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                        'tissue_type="corpora quadrigemina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              one="B23010402;
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                                                                                                                                                                                                                                                                                                            _stage="adult"
                                                                                                                                                                                                                                                                                 host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                 "male
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REFERENCE
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                                                                                                               P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kiuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.
           RIKEN Mouse ESTs (Konno, H., et al.) Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                         BB252299 312 bp mRNA linear ES BB252299 RIKEN full-length enriched, 7 days neonate ce musculus cDNA clone A730050L03 3' similar to AK000697 cDNA FLJ20690 fis, clone KAIA2769, mRNA sequence.
                                                                                                                                                                                                                                                         Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                       Suzuki,H., Suzuki,H., Tagawa
., Tsunoda,Y., Watahiki,A.,
                                                                 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K.,
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source N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoscitvation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), S20-524 (1988)

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The Institute of Physical and Chemical Research (RIKEN) Automated filtration-based high-throughput plasmid preparation yystem. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y. URL: http://genome.gsc.riken.go.jp/ Contact: Yoshihide Hayashizaki Please visit our web site (http://genome.rtc.riken.go.jp) for High-efficiency full-length cDNA cloning, Methods Enzymol, 303, 81-45-503-92 81-45-503-9222 genome-res@gsc.riken.go.jp, details Hayashizaki, Y Location/Qualifiers 1, .312 Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Sasaki

FEATURES

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                                                                                                                                                                                                   Sequence Tagged Connector Plate: 2191 row: N colu Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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1 (bases 1 to 411)
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                                                                                                                                                                                                                                                                                              Queen Anne Avenue North, Seattle, (206): 616-3618 3 (206) 616-3887 11: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ler, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
                                                                                                                                    quality sequence stop: 411.
Location/Qualifiers
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                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
'clone="Plate=2191 Col=24 Row=N"
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/dev_stage="7 days neonat
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Pred. No.
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21;
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BF588219
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genomics and Bioinformatics The University of Georgia, Department of P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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FM1_39_B06.b1_A003 Floral-Induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clade; Panicoideae; Andropogoneae;
1 (bases 1 to 435)
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciences Building, Rm.
                                                                                                                                                                           /note=Torgan: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhOI; Site_2:
ECORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda ZAP II. Clones to be sequenced were prepared by
mass excision."

87 t
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1 108 c 100 g 103 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum propinquum"
/db_xref="taxon:132711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Floral-Induced Meristem 1 (FM1)"
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Pred. No. 6.9e
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m. 2502, Athens, GA 30602-7271,
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. 6.9e+02;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 150)
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-MRO-CT0452-041100-303-h10 CT0452
                                                            Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rel: 864 656 5737
Fax: 864 656 4293
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                                                                             men
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       emson University
10 Jordan Hall, Clemson Universiy, Clemson, SC 29634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             emson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               one mgxb0009D16r,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ass: BAC ends
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                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              blast is an important model lumgar polynomerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 19216 clones with an average insert size of 130 km was constructed. This library represents greater user to the was constructed.
                                                                                                                                                                                                                                                                                                                                                                                                                                 than 25% genome coverage. High density are available upon request."

a. 156 c | 170 g 206 t 1 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of rice world wide. I a haploid genome (n=7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII, Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="mgxb0009D16r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Magnaporthe grisea"
strain="70-15"
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issue_type="Protoplasts"
ab_host="E. coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:148305"
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                   Catarrhini; Hominidae; Homo
                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                        7.6e+02;
hes 0;
                                                                                                                                               Homo sapiens cDNA,
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2 GTCTTTCGCAGATCGGTACCTCAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 150.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagai,M.A., da Silva,W.-Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-CT0452-
041100-303-h10&t3=2000-11-04&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     boratory of Cancer Genetics
dwig Institute for Cancer Research
a Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tact: Simpson A.J.G.
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence start: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl.
                                                                                                                                                        Note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CT0452"
                                                                                                                                                                                                                                                                                                                                                                                                    /órgànism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                      'dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         da Silva,W.-Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                  67.7%;
83.3%;
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                                                 0;
                                                                    Score 17.6; DB 12; Pred. No. 8.5e+02;
                                                 Mismatches
                                              Indels
                                                                                        Length
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                                                                                           150;
                                            0;
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                                            Gaps
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                                              0,
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밁 δÃ Matches 89 GTGTCTGGCAGATCGGCACCTCAA 66

Search completed: July 11, Job time: 474.474 secs

2003, 02:26:05

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GenCore version 5.1.6
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27: em_sts:* 28: em_un:* 29: em_vi:* 30: em_htg_lnun:* 31: em_htg_lnun:* 32: em_htg_other:* 33: em_htg_other:* 34: em_htg_pln:* 35: em_htg_pln:* 36: em_htg_pln:* 37: em_htg_van:* 38: em_sy:* 40: em_htg_o_hum:* 41: em_htgo_dus:*	18: em_in:*  19: em_on:*  20: em_on:*  21: em_or:*  22: em_ov:*  23: em_pat:*  24: em_ph:*  25: em_pl:*	 4: 9b_on: * 4: 9b_on: * 5: gb_ov: * 6: gb_pat: * 7: gb_ph: * 8: gb_p1: * 9: gb_pr: * 11: 4b_of: *	Post-processing: Minimum Match 1008  Maximum Match 1008  Listing first 45 summaries  Database: GenEmbl:*  1: gb_ba:* 2: gb_htg:* 3: cb_i:*	Total number of hits satisfying chosen parameters: 4109280 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 2054640 seqs, 14551402878 residues	Title: US-10-087-631B-9 Perfect score: 28 Sequence: 1 cgttcgtgggatagtccgtcatggtgtt 28	OM nucleic - nucleic search, using sw model  Run on: July 10, 2003, 18:15:27; Search time 242.625 Seconds  (without alignments)  3358.597 Million cell updates/sec	Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

C 45	44	C 43	. 42	٠.	c. 40	ω	c 38	w	ω	35	w	c 33	ω	w	30	c 29	28	c 27	∵ Ν	25	C 24	23	c 22	21	N	c 19	18	c 17	16	c 15.	<u>, , , , , , , , , , , , , , , , , , , </u>	_,	. د	110	٠.				, n,	י ת	4	ا سا	n N	_	NO.	Result	
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## ALIGNMENTS

REFERENCE AUTHORS	ORGANISM	KEYWORDS SOURCE	VERSION	DEFINITION	AC125937 LOCUS	RESULT 1
Rattus.  1 (bases 1 to 193862)  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	HTG; HTGS_PHASE1.	AC125937 AC125937.1 GI:21671543	orvegicus clor ered pieces.	AC125937 193862 bp DNA linear HTG 11-JUL-2002	

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Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisia, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill; R., Gabisia, C., Gavara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Helmandez, O., Hedgson, A., Hogues, M., Holloway, C., Hollins, B., Jackson, E., Huber, J., Hulk, S., Hume, J., Jackson, L.E., Varobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., C., Lewis, L., Li, J., Li, K., Lichtage, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Majue, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Mgyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwonu, G., Wetzker, M., Okuonu, G., Wetzker, M., Peters, L., Pickens, R., Primus, E., Pythus, E., Martindale, M., Okwonu, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                        Center project name: GH230-11B2
Center clone name: CH230-11B2
Center clone name: CH230-11B2
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 143063 bases at least Q40
Consensus quality: 151194 bases at least Q40
Consensus quality: 158097 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 193862)
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Direct Submission
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Buhay, C., Burch, P., Burkett, C., Bu
Carron, T.F., Carter, M., Cavazos, S.
                                  consists
                                                                                                                                                                                       NOTE: Estimated insert
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Earnhart, C., Edgar, D., Edwards,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
TE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
TE: This is a 'working draft' sequence. It currently nsists of 57 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to 193862)
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cha,S., Durbin,K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christopoulos,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ayele, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nelson, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escotto, M.,
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Bryant,N.P.,
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1224: contig of 1224 bp in length 1225 1324: gap of unknown length 2581: contig of 1257 bp in length

58338 80609 55845 49048 46531 43582 38034 10450 12259 12359 14970 16977 13642 13742 14870 gap of gap of gap of contig contig gap of contig gap of contig conti gap of contig contig gap of gap conti gap gap gap gap cont gap cont cont gap gap ( Cont unknown of 2570 unknown of 2027 g of 2849 f unknown g of 2517 of 3716 of. of 2293 unknown unknown of 1663 유 of 1809 of 1380 4570 length bp in length length bp in ] bp in length length ď length bp in length ģ đđ length nt dq length length length bp in length bp in length length length length length length Length length length Length length bp in length ength eng ength length ength ength .ength length 1 5 15 length length length length length length Length length length length Length length length length length . length length length length length length length length length length length length length length

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ORGANISM
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                         Ng,W.V., Kennedy,S.P., Mahairas,G.G., Berquist,B., Pan,M.,
Shukla,H.D., Lasky,S.R., Baliga,N., Thorsson,V., Sbrogna,J.,
Swartzell,S., Weir,D., Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
Leithauser,B., Keller,K., Cruz,R., Danson,M.J., Hough,D.W.,
Maddocks,D.G., Jablonski,P.E., Krebs,M.P., Angevine,C.M., Dale,H.,
Isenbarger,T.A., Peck,R.F., Pohlschrod,M., Spudich,J.L.,
Jung,K.-H., Alam,M., Freitas,T., Hou,S., Daniels,C.J., Dennis,P.P.
Omer,A.D., Ebhardt,H., Lowe,T.M., Liang,P., Riley,M., Hood,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                              3 TTCGTGGGATAGTCCGTCATGGTGT 27
                                                                                                                                                                            Halobacterium sp. NRC-1.
Halobacterium sp. NRC-1
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                  DasSarma,S
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Pred. No. 4
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                           Hou, S., Daniels, C.J., Dennis, P.P., Liang, P., Riley, M., Hood, L. and
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20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-JUL-2000) Institute for Systems Roosevelt Way NE, Seattle, WA 98105, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jung, K.-H.,
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Shukla,H.D., Lasky,S.R.,
Swartzell,S., Weir,D., E
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Ng, W.V., Kennedy, S.P.
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                                                                                                           complement(1928...2224)
/gene="VNG1425H"
complement(1928...2224)
/gene="VNG1425H"
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601. .1512
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/db_xref="GI:10580926"
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LANVAYGSDGLDLLRAGHSADEVVAELTNTDDEAPQRQVGVVGQDGSVAAFTGAECVD
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/db_xref="GI:10580925"
                                                               transl_table=11/
                                                                            codon_start=
                                                                                            /note="hypothetical protein"
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.SDALTARESFMNTAGVRRPDGSYVVERRGADSAGNRKVFESFDALRGRCRRPPETFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:64091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain="NRC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Halobacterium"
translation="MTETVLFESESTQSRADVAAYLRTVADNLQNNDTITLSAGGDTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keller, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "VNG1420H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D., Hall, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mahairas,G.G., Berquist,B., Pan,M.,
L., Baliga,N., Thorsson,V., Sbrogna,J.,
Hall,J., Dahl,T.A., Welti,R., Goo,Y.A.,
K., Cruz,R., Danson,M.J., Hough, M. Dale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 (22), 12176-12181 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp. NRC-1"
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
/transiation="MSAGEHAGGVFLGGIAIDEPTREAARAMYDRDREEFLPADPVAW
VDDQLSELDDAFLAPAVNVBAVRLGPLRDVAAVCAAHDAILEVNAHCRQDELCDAGAG
ETLLRDTSRLCEQVRAASDEGAAVSVKVRAGVQGVHLPVLAQAIERAGAAAIHVDAMD
                                                                                     /product="Vng1431c"
/protein_id="AAG19744.1"
/db_xref="GI:10580932"
                                                                                                                                                                                                                                                                                                                                        TAGVADAYDFADAFVLDTADSTDLDRPVVRTDTSLDTEADAERVARACRDALVAASGE
                                                                                                                                                                                                                                                                                                                                                                 PMSNDPVATIVQTPDGEQHFQTFWVAEHGDPTVEDVEFRGGERATAAQPAIEAIRDGP
VVVGPSNPVTSIGPMLALDGIADALRDAQVVAVSPFVEDEVFSGPAAKLMAAVGHDPS
                                                                                                                                                                                                                                                                                /gene="VNG1431C"
                                                                                                                                                            transl_table=11
                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                               'note="conserved hypothetical protein"
                                                                                                                                                                                                                                     gene="VNG1431C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Vng1427h"
/protein_id="AAG19741.1"
/protein_id="AAG19741.1"
/db_xref="GI:10580929"
/translation="MVAARLATAAVGVAGSLAVSVVAWQVFDLPVFVLAVPFVPFLFR
RRGBGSSPRTRRCPECGFTTRTPSVTHCPHDGTELD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FVVHFARLVLPELVAGEGIAPVPAGADDTPASDADPESAADPDDTAA
                                                                                                                                                                                                                                                                                                                                                                                                            PDLDTVLFEGGGVLDRETWWGIADDGSTTHDYLTDLAAAADIDPDTPRYLPDDAOTA
RDIARWRRESAASEFMFIGDRDRAVHTLRAGLLDEGHTLTEVTRRLADAFDLSVDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="VNG1429C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPVYRRVDRHLRSSSVAAVVSLLVLALPVVYLLSYTTAVGIQELTRVLNAPQIDLTT
TBALVQPYVDVSRAVQDPQSLLGQPSVRAAINTTLRSAGQYAGFLGTAFYHLFAVTTI
NFYLLRDDTRLAEWFHSRFADSDGVVRAYTAAIDADFSNIFFGNILFAFTTGVIASIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2886. .4034)
/gene="htlA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="Htr-like protein"
protein_id="AAG19742.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNLDTLVEKGLIDKGELDQRTNYYTLTHRGTRELEARREWETQYVGQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="VNG1427H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein_id="AAG19740.1"
'db_xref="01:10580928"
'translation="MHDLTGFQRDLLYYVAGLDEPHGLAIKDELEQYYTSEIHHGRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVDPPASVDFEVKAERETTGGSGPDELSIEFELEWDDADHSADGETTDTGLDIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="Vng1426h"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ranslation="MGDTRIDRGRAAWWAIGATLTAALVYVVYTFVGTFVLGFFLYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cotein_id="AAG19742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             duct="Vng1429c"
tein_id="AAG19743.1"
.xref="GI:10580931"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQIVFPSSLSIPYPTLMGLLTGAASLIPVVGIKLVWIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e- "VNG1428G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ation="MTTFLAGGTGTPKLLAGARRVFDPAETTVVGNTGDDVALGGLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'NG1'429C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'NG1427H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'GI:10580930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4034)
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VERSION
KEYWORDS
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AC119388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3946 CGTTCGTGGGAACGTTCGTCCTGGGGTT. 3919
           Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davilla, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Elagy, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Sarilei, N., Serraguto, D., Serraguto, D., Flagg, N., Ford, J., Ford, J., Serraguto, D., Serraguto, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                 Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T. Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 187487)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC119388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 187487 bp DNA norvegicus clone CH230-215C17, ***
       Gao, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVRNRIAGYITHKRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSGSLTEDIIKTAKPFKMGEWDVDEAALREEGINRLGNIFVPSDRYVWLEEYLYDFFB
EFFADQKVRPPTAFARELGATLDDEDSILKNAADNDIPVFCPALTDAEIGNFLYYYRQ
GYDSEVGIEILDDYDALIEEGLLADTTGLICVGAGVPKHHAIMTNLFRGGADYAYYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MAIKPDYVKKTGNILMERYQDAFSREDFEHNKDAVTELTNIESK/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Rps17e"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGFQASHLADAVDITREMREDDATIYLTLTSNIVSSGLREVVAHLVRENYVDVIIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="GI:10580934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="rps17e"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="VNG1433G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="rps17e"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMEGDGSLSGAPPEEAVSWGKIKDEDAEPNYALIEAEATLVFPLLVAGAFENP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MTGDDADETHENVVPGSDEDLDTPDVRGYDFSGEFDFFELLDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="deoxyhypusine synthase"
protein_id="AAG19745.1"
db_xref="G1:10580933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;000. .6992
/gene="dhs"
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Baylor Plaza, Houston,
3 (bases 1 to 187487)
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Direct Submission
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                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                       as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-215C17
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Center clone name: CH230-215C17
Center clone name: CH230-215C17
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; versiton 0.990329
Consensus quality: 146444 bases at least Q40
Consensus quality: 153280 bases at least Q30
Consensus quality: 157543 bases at least Q20
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COMMENT

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                     Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                               Center: Washington University Genom Center code: WUGSC
                                                                                                                                pirect Submission
Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
(bases 1 to 191844)
McPherson, J.D. and Waterston, R.H.
                                                                                       Parkway, St. Louis, MO 63108, USA
On Jul 5, 2002 this sequence version replaced gi:21105870.
                                                                                                Direct Submission
Submitted (05-UUI-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                         1 (bases 1 to 191844)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus. musculus clone
                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                          AC122410 191844 bp DNA linear HTG 05-
Mus musculus chromosome UNK clone RP24-142A1, WORKING DRAFT
                                                                                                                                                                                                      (CPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                  unpublished
                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                         sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; dammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                        iouse mouse.
                                                                                                                                                                                                                                                                                                                                              AC122410.2 GI:21699728
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enter project name: M_BB0142A01
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     153158
              2 GTTCGTGGGATAGTCCGTCATGGTGT 27
 GTTTGAGGGACAGTCCCTCATGGTGT 153183
                                                                                                                57770
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COMMENT

Gaps

0;

REFERENCE

AUTHORS TITLE

REFERENCE AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS TITLE JOURNAL

VERSION KEYWORDS

ORGANISM

ACCESSION

RESULT 4 AC122410

LOCUS

DEFINITION

В

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Similarity
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Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 18883 bases at least 040
Consensus quality: 189311 bases at least 030
Consensus quality: 189313 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 0.00 in Q20 bases; agarose-fp Quality coverage: 11.99 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 193000
Insert size: 192017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
   Conservative
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18750
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1286
2467
2567
8025
                                                                                     /note="assembly_name:Contig8" 38253 c 38232 g 56888 t
                                                                                                                                              vector_side:left"
                                                                                                                                                                            82873. . 191197
/note="assembly_name:Contig28
                                                                                                                                                                                                                                            191298. .191844
                                                                                                                                                                  clone_end:SP6
                                                                                                                                                                                                                                                                                                                       8125. .18649
                                                                                                                                                                                                                  /note="assembly_name:Contig27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-142A1"
                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig22"
                                                                                                                                                                                                                                                                                               note="assembly_name:Contig25"
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192017; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                         assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : gap of unknown length
: contly of 10525 bp in length
: gap of unknown length
: contly of 23604 bp in length
: gap of unknown length
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: contly of 40319 bp in length
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of unknown l
contig of 1181 b
gap of unknown l
contig of 5458 b
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
               Score 19.6;
Pred. No. 99;
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Mismatches
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lg of 108325 bp in length
of unknown length
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                     Length 191844;
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone T28A8. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-1997) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode wustl.edu on Jun 13, 1998 this sequence version replaced gi:1877160. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a sma overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The true right end of clone Y43F4 is at 14666 in this sequence. The true right end of clone T27E9 is at 16930 in this sequence. The start of this sequence (1...104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consorscience 282 (5396), 2012-2018 (1998)
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For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end of this sequence (34285. .34388) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   true right end of clone T28A8 is at 104 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
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                                                                                                                                                                                                                                                                                                                                 complement
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="III"
                                                                                                                                                                                                                                                                        /gene="T28A8.1"
                                                                                                                                                                                                                                                                                                                                                       /clone-"T28A8"
                                                  /protein_id="CAB07286.1"
/db_xref="GI:3880336"
                                                                                                                                                                                            'gene="T28A8.1"
                            'db_xref-"SPTREMBL:Q9XU07"
                                                                                                             codon_start=1
                                                                                                                                       note="contains similarity to Pfam domain: PF02034 (TASK + channel), Score=-80.4, E-value=3.4e-05, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers.
translation="MATWKTYARIILAHVSLIVLSVVYVGFGAFLFYQLEQPNEVEVR
                                                                                                                                                                                                                nent(join(2569. 2659,2830. 2990,3030. 3467,3861. 3951,3998. 4197,4279. 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34388 bp DNA linear LNV cosmid T28A8, complete sequence.
                                                                                                                                                                                                                   ..2659,2830. .2990,3030.
51,3998. .4197,4279. .43
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                                                                                                                                                                                                                   030. .3099,
.4397,4889.
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.4397,4889.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
for a small
                                                                                                                                                                                                                                                                                                  .5105))
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  gene
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HLRPGGEDEDYNWTYMTALFFTTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPLILI
TVADIGKFLSENIVQLYTWYRKLREKCSKQKYSVISSKDDKNKEGDLNLDHLENYISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="T28A8.2"
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/gene="T28A8.5"
                                                                                                                                                                                                                                                                                                                                          QEMMIEDNNSSISERNADVPFVEHQQISLSAESRDTSAESESIYLHDFLKQLAQFISF
FECSELAEIKKNIKEVMADEEKIAGFQKVKILDIRTVLGAFFFGVSRKIKSTGSNNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRDASQEDKEVSSNWPVYNKTSFGDDMEYIGAVKGQPKPEPIDFDFYQINNREHFQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKVFAEFSENGGGGRTDQAYYKQFRRRVAPKMAKLKEYSIHDRVRVMFGLSGQVSNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RICKYTSDEGNLSLEGIHCKSSEAVRKRSTNATLSADFVRLMTFLTEKTKDSIKPLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mylkeadskremkflyngtkgavkplypttvfrkfaklkgselg
atayanrfenylypnmdkmneysielrirvmfgmsakvsndflegikttgtvqvdelg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA EST yk617f9.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEFLVLNETVPDQVVWVDFNRKCCTFENPQKLKNWKLQENEIIYLTGLYYQSFKYFPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIFLIVAILLSYITFGAVVLSMWEGWDFFSGFYFSFITMTTVGFGDIVPLKREYYILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARNIERFNIHKROMIEHLWEMRESGIGOHVVEDLAVKYVDNVTRILFEAFDTHCIGAK
                                                                                                                                                                                                                                                                            MKVKDFMFKFKFFLLGLDCSELLELQQKVHEKLDEQDVTKKILLYSDIQKALQSLIYT
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/translation="MIIVSRGFSLYFFLLWTFLLVLVVYFYTLLPENEVNGTPVFEER
                                                                                                                                         oin(17556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="SPTREMBL:Q9XU04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="GI:3880339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="CAB07289.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"cDNA EST yk617f9.3 comes from this DNA EST yk617f9.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oin(15151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSKGNQVYYADIRGTNDSVYKTGDLKPDDYYLPHWIPVKVEADIFSYRNFFKKKIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQQKYGQKKTHDTIIVKGAYAPKDLSKIRFIDFGALASIESWQSLWSILTGRTQEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIVQLDDNRRICKFVSHDGKLKLEGNRKNSARVERRSAKNRDPGANATRQY
                                                                    556. .17713,17762. .17875,17921. .18068,18116. .1
.18914,18959. .19072,19121. .19215,19284. .19384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151. .15302,15347. .15460,15505. .15786,15830. .15943
.16215,16267. .17200,17251. .17313)
                                                                                                                                         .18550
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HSEDYYVRRFHRKLAPKMARWDNFSIEARVRLMFGLDGKVADDFLRQIRIYGAVQLDE NRRICHFTSHDGQVKLESTELTELKQQVKEKIGTDDADSLQITDLRTVFEAFFVGISR

translation="MATTSTELSREMSELVEQVNDATEPMTVQRVFTQESQLGAGV"

/protein\_id="CAB07285.1" /db\_xref="GI:3880335"

'db\_xref="SPTREMBL:Q9XU08"

/gene="T28A8.

'note="predicted using

/codon

join(17556. .17713,17762. .17875,17921. 18802: .18914,18959. .19072,19121. .j92

.,19215,19284. .19384)

18068,18116.

.18550

KIKSSAPNNSTSTISAKDYLLKENFILLGLDCSEFRELOOTVERKINDPBIANKVETIN RVKPIKKMNLFAGSSDORHTPSSSRPALLHFTLILIFFGETCLESPFFFESVVFSLII VISTISCEOSKRORIPLSHWMYQKCSONTVITNRENDGSYNVYYDRFHHHLAPKAAK

LEEYSIVERVRVIFGFAGKVSNDFLKQIRREGIVELDKKKQICKFSSHDGKVKLQGDH

.20240,20286.

.20399

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RESULT 6
DDIGP100/c
                VERSION
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                                                                  DEFINITION
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                             Dictyostelium of complete cds.
           L04286.1 GI:167796
                                                                                 DDIGP100
                                                                                                                                                                TGGTGGGATATTGCGTCATGGTGT 13920
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                        TCGTGGGATAGTCCGTCATGGTGT 27
                                                                                                                                                                                                                                        Conservative,
                                                                                                                                                                                                                                                                                                 complement(join(25273...25524,25935...27554...28040,28831...28939,29088...;
30318...30496,30663...30714))
/gene="T28A8.7"
/note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPKLAEIKOOIKESIGTGEDEKLOVTDIHTVLEAFFFGVSRKIRLDASNNPAMKVKDF
TLKFKFFILALDFSELLELKKKVOGIIDEPEFNEKILPISDIRRSLONLLFTISO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYLTEYSKRENDGLSYSYYYRRFRRSVAPNMAKFENYSIEERVRIMFGFAGKVADDF
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/gene="TZ8A8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYSRFHEHIAPNIGKCNNFNVYTRIRMFALSATVPDSFLALIRFTGTVQLDERKRIN
KYVSNDGRLNLEGYHRCMARSKNQWGKDPAEVTRLMNFLVEKAKDSIEPLVATAVFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MVFTDTQLERLMSFLVEQTKDSIEPLVVLKVFTEYSNRENDGLS
REYYDRFRTSVALNMAKLTEYTIEDRIRVMFGFAGEVSDDFLTKIETIGIVKLDEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id="CAB07287.1"
db_xref="GI:3880337"
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db_xref="GI:3880338"
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A EST yk599h7.3 comes f
A EST yk599h7.5 comes f
A EST yk599h7.5 comes f
                                                           discoideum
                                                                                                                                                                                                                                                       68.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                             lement(join(25273. .25524,25935. .26477,2699
4. .28040,28831. .28939,29088. .29256,29951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA EST yk215a12.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .20593,20651. .20987,21035.
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                                                                                                                                                                                                                                                       Score 19.2;
Pred. No. 1.
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                                                                         1841 bp
                                                                                                                                                                                                                                      Mismatches
                                              glycoprotein gp100 (P29F8; GP100) mRNA
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.20987,21035. .21250
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                                                                           linear
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.29256,29951.
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.23965,24012. .24227,
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.21250,21299. .21364)
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                                                                      INV 14-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                         .30164
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TITLE
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SOURCE
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AE004745
LOCUS
                                                                                                                   REFERENCE
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                                                                                                                                                                                                                                                            ACCESSION
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AUTHORS
TITLE
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AUTHORS
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Best Local ;
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                   472 GTTGGTGGTATAGTTTGTGATGGTGTT 446
Stover.C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                              ĀE004745 AE004091
AE004745.1, GI:9949336
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                    Pseudomonas.
                                                                                                                                                                                            Pseudomonas aeruginosa.
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Muller-Taubenberger, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barth,A., Muller-Taubenberger,A., Taranto,P. and Gerisch,G. Replacement of the phospholipid-anchor in the contact site A glycoprotein of D. discoideum by a transmembrane region does impede cell adhesion but reduces residence time on the cell s. Cell Biol. 124 (1-2), 205-215 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-OCT-1992) Annette Muller-Taubenberger, Max-Planck Institute for Biochemistry, AM Klopferspi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein; glycoprotein gp100; transmembrane protein. Dictyostelium discoideum cDNA to mRNA. Dictyostelium discoideum Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                                                                                                             (bases 1 to 11884)
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4.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICELSKSYHTLSSPKTTNTTMLSFINNSPNSTVSNEIIEMISGYFQIKISTKPSTTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCYANPIIDKVIGYKDKKLTLITIIGKNFLNNATVIIEKPNGNKRNCSNVLLSTDTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTDDYEPSIKIGNKICETLTSSQTSIRCYLTNGTGCGYTITIDNLLNPIDNNGNSNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIIKFNITDIEDIEMGKITISYKNGQSSSKHFQPNSIIKSIERTNSVGGVVEFKGSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIIISGHFSIDKTGLTVTYLGDKIHDFEFIKGQVLNVTGEPQNNPIPTVSINPDQLND
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STPTPTSTPTPTSGTIPPTSQTIPPPTTTPKPTSKPTSKPTSKPTSKYSKGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard_name="P29F8; GP100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone_lib="lambda gtil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="lambda-cDP56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No.
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                                                                                                                                                                                                                                                                                      11884 bp. DNA linear BCT 30-AUG-2000 PA01, section 306 of 529 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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1.5e+02;
5;
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Complete genome sequence of Pseudomonas

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CDS		gene
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gene	VRLETORKKLTVFFSDIRGFTELSEELEAEALTDLLNNYLNEMSKIALKYGGTIDKFV	
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CDS		gene
	``	
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•	Loca	FEATURES
•	n Genome Center, Univer	
	Submitted (16-MAY-2000) Department of Medicine and	JOURNAL
	Direct Submission	TITLE
	u,Z., Paulsen,I.T., Reizer,J., Saier,M.	0
	Vadman,S., Yuan,Y., Brody,L.L., Cou Vadman,S., Yuan,Y., Brody,L.L., Cou	
	Barber, R.L., Goltry, L., Tolentino,	
CDS	STOVET,C.K., Pham,XQ.T., ETWin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik.D.J.,	AUTHORS
gene	2 (bases 1 to 11884)	REFERENCE
	20437337 10984043	MEDLINE
:		JOURNAL
_	Opportunictio mathomom	

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LAHSLFVASLAVVKARTAALVFALEFVYGIAFAWLLFHETPGPRWFLGGALIILAIVL
                                                                                                                                                                                                                                                                                                    SARLGARGRKTAVGDERGDPERA"
                                                                                                                                                                            complement(6206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRIEGYDYLNCGDWVESCTALIEHWDGSIQLYRLAEEQARLAAQAAAVEPAA"
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                                                                                         transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="PA3220"
                                                                                                                        codon_start=1
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GFVGIHDVTFIHAEGMNMGPEFREKGLARARERMRQALETDTSLCVPLPTLR"

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COMMENT
                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                               KEYWORDS
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                                                                                                                                                                                                           TITLE
                                                                                                                                                        AUTHORS
                                                                                                                         JOURNAL
                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                 Direct Submission
Submitted (09-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
     Web site:http://genome.wustl.edu/gsc/index.shtml
                             Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                    1 (bases 1 to 14687)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clon
                                                                                                                                                                                                                                                                                                                    AC126800.1 GI:21717270
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                           AC126800 14687 bp DNA linear HTG 09-J
Mus musculus chromosome UNK clone RP24-447D19, WORKING DRAFT
SEQUENCE, 10 unordered pieces
                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                    cPherson, J.D. and Wa
                                                                                                                                                                                                                                                                         šukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                             iouse mouse.
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                                                                                                                                                                                                                                                                                                                                                                   10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="peptidyl-prolyl cis-trans isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QROLGVPILRIDGRKAVLTEAGEVLLRRSRQLVKQAGQLEELAHHMEQGWEPEVRLVV
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7511. .8440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="PA3226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /genė="PA3225"
                                                             ---- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAEQAGLREKIEARWAENDKRAYLASLDAIIGWGVQERLAEIACPTLVISADRDYTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lb_xref="GI:9949347"
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                                                                                                                                                 and Waterston, R.H.
                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              !ADARLVVVEDSRHATPMDQPEIFNTTLLGFLADIDKTKEQPCSNVS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 1;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                    clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcriptional regulator"
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 11865 bases at least Q40
Consensus quality: 12505 bases at least Q30
Consensus quality: 13903 bases at least Q30
Consensus quality: 13903 bases at least Q20
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puality coverage: 1.48 in Q20 bases; sum-of-contigs
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Insert size: 13787; sum-of-contigs
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13235. .14687
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Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (11-MAR-2002) Genome Sequencing Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington C
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22; Conser
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Submitted (30-MAR-2002)
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The sequence of Homo sapiens
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                        Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name:
                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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as compressions and repeats; from more than one subclone; restriction digest all regions were covered by sequence and the assembly was confirmed by

MAPPING INFORMATION:

sequence, see http://genome.wustl.edu/gsc Mapping information for this clone was provided by Dr. John D McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this ō Louis

SOURCE INFORMATION:

donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenteteno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome Research Genetics, Inc. (http://www.roand.org The RPCIibraries. pBACe3.6 Genomics 51:1-8. The clone may be obtained either human BAC library was made from the blood of one male (http://www.resgen.com) or Pieter Zhao, B., Frengen, E. de Jong from

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-25B14, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-603P13;
actual end is at base position 101783 of RP11-25B14.

Location/Qualifiers

FEATURES repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region source repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region /rpt\_family="AT\_rich" 13582. .13621 /rpt\_family="AT\_rich" 12037. .12066 /rpt\_family="(TATG)n" 733. .839 /clone="RP11-603P13" /clone\_lib="RPCI-11" 12498. /rpt\_family-/db\_xref="taxon:9606' organism="Homo sapiens" rpt\_family-"L1" \_family-"MIR" \_family="AT\_rich" \_family="AT\_rich" \_family="MIR" \_family="MIR" \_famil \_tami \_famil \_family="L1" tami family="MIR" familyfamily="L2" family-"L1" family-"(CA)n" . 6075 .11826 .11313 y="MIR" Ly="L1" y="L1" y="Alu" "ERV1" "(TAGA)n"

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality data (i.e., phred quality data).

problems, such

quality

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

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GTTCGTGGGTGTGTCCGTGAGGGTGTT 54199

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576. .22017
                          67.9%; Score 19; 81.5%; Pred. No. 1
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                  Mismatches
              DB 9;
1.9e+02;
5;
                                 Length 80015;
                 Indels
                ۰,
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REFERENCE
AUTHORS
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                                                                                                          Direct Submission
Submitted (21-DEC-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                  University, 4444 Forest 3 (bases 1 to 115045)
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                                                                                                                                                                                                                   Submitted (20-MAR-1998)
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                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 115045)
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Homo sapiens PAC clone RP4-724E13
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            Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
Center project name: H_DJ0724E13
                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                         Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA linear PKL 21-1 from 7p11.2-p12, complete
                                                                                                         Washington
Missouri 63108,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was by restriction digest.

Project (Eric D: Green, Director), John D. McPhe Department of Genetics (Washington University), University Genome Sequencing Center. For additiabout the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genc MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping. Project (Eric D: Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington Trainersity Genome Sequencing Center. For additional information

see http://genome.wustl.edu/gsc

# SOURCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP4-537J23. Actual start of this clone is at base position of 1 of RP4-724E13; actual end is 115045 of RP4-724E13. This clone was derived from human PAC library RPCI-4, prepared by Pleter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For further details, see http://bacpac.med.buffalo.edu/
The clone is available from Genome Systems, Inc. (http://www.genomesystems.com).

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. Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="7"
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2. .16727
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_family="L1"
2. .17261
                        _family="Alu"
4. .16809
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LOCUS AC120560 123770 bp DNA linear HTG 18-JUL-2002 DEFINITION RATTUS norvegicus clone CH230-330L5, *** SEQUENCING IN PROGRESS
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17262. .17711
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                                                                                                                                    Score 19; DB 9;
Pred. No. 2e+02;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Direct Submission
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GTUZ
Center clone name: CH230-330L5
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Buhay, C., Burch, P., Burkett, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                  Jul 14, 2002 this sequence version replaced gi:20514410
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 96476 bases at least Q40
Consensus quality: 99583 bases at least Q30
Consensus quality: 101766 bases at least Q30

**NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

**NOTE: This is a 'working draft' sequence. It currently
consists of 29 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.

**This record will be updated with the finished sequence
be preserved.

1038: contig of 1038 bp in length
1138: gap of unknown length
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60471 60571 67471 67571 72024 72124 82883 53059 40595 44085 23370 10988 11088 12209 12309 gap o conti gap o conti gap o gap of gap c gap gap Conti conti gap o contic gap o gap o gap o gap of conti gap o cont cont. gap o gap o y of 10759 bp in y of 6123 unknown of 2072 f unknown of 2168 unknown of 4453 unknown of 4347 of 3538 of 2929 of 2246 of 1866 unknown 4122 4652 3421 bp in length length length þ bp in length g đđ bp in lengt bp in length bp in length length length length length bp in length Length bp in length ďď length length bp in length ength length bp in bp in length bp in length ength Length length .ength length Length length length ength ength length 
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Best Local Similarity
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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Scher, S., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstok, G., and Gibbs, B.
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Rattus norvegicus
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98184: gap of unknown length 123770: contig of 25586 bp in length.
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Pred. No.
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2e+02;
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, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hernandez, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jul 9, 2002 this sequence version replaced gi:17941355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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NOTE: This is a 'working draft' sequence. It currently
consists of 75 contigs. The true order of the pieces
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be preserved
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AC117647/c
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Best Local
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                                               McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Vassillev, H., Theodore, J., Topham, K., Travers, M., Vassillev, H., Vassill
                                                                                                                                                                                                                                                                                                      Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 1795/2)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J. Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Mus musculus clone RP23-244M7, WORKING DRAFT SEQUENCE, 22 ordered
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Wilson,B., Wu,...
and Zody,M.
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Lindblad-Toh, K.,

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COMMENT

TITLE

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Smit, A.F.A. & Green,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provided by the submittor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is believed to be correct as given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 172421 bases at Consensus quality: 175743 bases at Consensus quality: 176806 bases at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 5.0 in Q20 bases; Quality coverage: 5.1 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye; 100% o Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead
106966 106965; gap of 100 pp
106966 119527; contig of 12562 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accession number will
                                                                                                                                     5026 85125: gap of 100 bp 5126 91380: contig of 6255 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     832 931: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                finished sequence as soon as it is available and
                                                                                                                      91480:
                                                                                                                                                                                                                                                                                                        52353: gap of 100 bp
56294: contig of 3941 bp in length
56394: gap of 100 bp
62939: contig of 6545 bp in length
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4649: cor
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                                                                            98976:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10116: gap of 100 bp
11576: contig of 1460 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2184: contig of 1253 bp in length 2284: gap of 100 bp
                                                                                                                                                                                                         75002:
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                                                           06865:
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                                                                                                                                                                                                                       2: gap of 100 bp 4902: contig of 7470 bp in length
                                                                                                                                                                                                                                                                                                                                                                                             9: gap of 100 bp
2253: contig of 37874 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                       6: gap of 100 bp
4279: contig of 2603 bp in length
                                                gap of 100 bp
55: contig of 7889 bp in length
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BASE COUNT
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'db_xref="taxon:10000"
'clone="RP23-244M7"
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2e+02;
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AC009921 LOCUS

REFERENCE

TITLE

KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

REFERENCE

AUTHORS JOURNAL AUTHORS

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Submitted (08-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 26, 2000 this sequence version replaced gi:6479138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Seve Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagne Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
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Baker,J., Baldwin,J., Barna,N., Beck
Castle,A., Cerny,J., Colangelo,M., C
Cooke,P., DeArellano,K., Depayre,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marguis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Paylin, B.,
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Funke,R., Gage,D., Galagan,J., Gardyna,
Hagos,B., Heaford,A., Horton,L., Howlan
                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                consists of 16 contigs. is not known and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karatas, A., Lehoczky, J.,
Marquis, N., McEwan, P., Mc
                                                                                                                                                                                                  be preserved.
                                                                                                                                                                                                             as soon as it is available and the accession number
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                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 187586; sum-of-contigs Quality coverage: 5.2 in Q20 bases; Quality coverage: 4.6 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.960731
Consensus quality: 179818 bases at least 040
Consensus quality: 183946 bases at least 030
Consensus quality: 185564 bases at least 020
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Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                 2211: contig of
1: gap of 1
     1: gap of 100 bp
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5: gap of 100 bp
5319: contig of 1604
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7164 24729: contig of 7566 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2507 12606:
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/note="assembly_fragment"
120589. .147913
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33004 c . 33086 g 59542 t
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                                                                                                                                                                                                                                                                                                                                                                        'note="assembly_fragment"
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'db_xref="taxon:9606"
'clone="RP11-115018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 5419: gap of 100
0 7668: contig of 2
9 7768: gap of 100
9 12506: contig of 4
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46466: contig of 10532 bp in
666: gap of 100 bp
61624: contig of 100 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09: gap of 100 pp
94997: contig of 17388 bp in
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77509: contig of 15785
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                            Score 19; DB 2;
Pred. No. 2e+02;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at http://www.sanger.ac.uk/Projects/Control Control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is the entire insert of clone RP11-512M17 The true left end of clone RP11-545P6 is at 121889 in this sequence. The true right end of clone RP11-315A9 is at 159267 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Nov 23, 2000 this sequence version replaced gi:11321907. During sequence assembly data is compared from overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL354896.16
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RP11-512M17 is from the library RPCI-11.2 constructed at the ROSWell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rresponding to the overlapping clone, as we submit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :p://www.sanger.ac.uk/HGP/Chr13
l1-512M17 is from the library F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a small overlap as described above.
                                                                                                                                     /note="Sequence from overlapping clone
bA315A9(AL162498).Assembly confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome="13"
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                                                                                                                                                                                                                                                                                                                                                                                 note="L1PA12 repeat: matches -55. .1238 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MSTA repeat: matches 160.
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   te="L1M2 repeat: matches 2455.
5. .4188
                                                                                                                                                                                                                                           e="L1 repeat: matches 2124.
                                                                                                                                                                                                                                                                                                        e="L1PA12 repeat: matches -1416. .-839 of consensus"
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m clone RP11-512M17 on chromosome
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   "AluSg repeat: matches .39269
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                                                                                                                                                                                                                                                                                      .35598
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1192. .4433
/note="Alusc repeat: matches 135.
                                           note="LIMA4 repeat: matches 5911 . 6299 of consensus"
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e="L1M2 repeat: matches -707...-278 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="Tigger3b repeat: matches 4. .1224 of consensus"
7. .18771
e="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                   e="Sequence from overlapping clone
5A9(AL162498) Assembly confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                    e="LIME repeat: matches 4978. .5229 of consensus"
5. .29844
                                                                                                                                                                                                                                                                                          e="MER2 repeat: matches 2. .344 of consensus"
                                                                                                                                                                                                                                                                                                                 =="L1ME repeat: matches 4297. .4914 of consensus"
5. .30415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ="L1ME repeat: matches 5318. .5765 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p="Sequence from overlapping clone
p="Sequence from overlapping clone
pag(AL162498).Assembly confirmed by restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ="16 copies 3 mer agg 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *AluSx repeat: .matches 1.
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). .12276
--"LLM3e repeat: matches -870. .-580 of consensus"
                                                                                                                                           ="AluJo/FRAM repeat: matches 157. .249 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -"MSTA repeat: matches 1. .177 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "THE1C repeat: matches 316...422 of consensus" ... 28487
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.308 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4115 of consensus"
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                                                                                              .6304 of consensus"
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                                                                                                                                                                                                                               /note="L1MD repeat: matches 83.
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39487. .39579
/note="MIR repeat: matches 166. .261 of consensus"
39604. .39737
/note="LIME repeat: matches 5308. .5443 of consensus"
40178. 40217
/note="0.00pies 2 mer ct 97% conserved"
                                                                                                                                                                        67.9%; Score 19; DB 9; Length 209743; 81.5%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ""L1MA8_repeat: matches 5148 .6287 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -"MLT1E
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A9(AL162498).Assembly confirmed by restriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ""L2 repeat: matches 1882. .2236 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "L1M4 repeat: matches 4141 .4604 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "LIMC3 repeat: matches 6701. .6810 of consensus" .44935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 2015, .2117 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 4538. .5260 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 2211.
                                                                                                                                                                                                                                                                                             8 repeat: matches 4787. .5125 of consensus<sup>*</sup>
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copies 2 mer ct 97% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 2612. .2691 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epeat: matches 1825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C repeat: matches 1. .369 of consensus
                                                                                                                                                                                                                                                          repeat: matches 6133. .6216 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copies 2 mer aa 63% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 repeat: matches 5746. .6108 of consensus"
                                                                                                                                                                                                                                                                                                                                           repeat: matches 177.
                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 1. .177 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pies 2 mer aa 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 5909. .6143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 9. .505 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 6868. .6900 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 repeat: matches 1. .278 of consensus
                                                                                                                                                            Mismatches
                                                                                                                                                                                                                          .708 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1735 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2054 of consensus
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                                                                                                                                                       Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                     Result
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                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Ap Serotype

## ALIGNMENTS

041	RESULT 1	CT 1
	ABQ41	1020
	IJ	ABQ41020 standard; DNA; 510 BP.
	<b>XX</b>	
	X AC	ABQ41020;
	DT	
	XX	
	DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 27611.
	XX	•
	W	<pre>Human; cytosine methylation; '5'-CpG-3'; uracil; cytosine; diagnosis;</pre>
	ΚW	<pre>drug; side effect; cancer; central nervous system; cardiovascular;</pre>
	ΚW	gastrointestinal; respiratory system; single nucleotide polymorphism;
Homo sapiens.  WO200218632-A2.  07-MAR-2002.  01-SEP-2001; 2001WO-EP10074.  01-SEP-2000; 2000DE-1043826.  05-SEP-2000; 2000DE-1044543.  (EPIG-) EPIGENOMICS AG.  Olek A, Piepenbrock C, Berlin K,	X	SNP; cell differentiation; ds.
HOMO Sapiens.  W0200218632-A2.  07-MAR-2002.  01-SEP-2001; 2001WO-EP10074.  01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543.  (EPIG-) EPIGENOMICS AG.  Olek A, Piepenbrock C, Berlin K,	2	
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07-MAR-2002.  01-SEP-2001; 2001WO-EP10074.  01-SEP-2000; 2000DE-1043826.  05-SEP-2000; 2000DE-1044543.  (EPIG-) EPIGENOMICS AG.  Olek A, Piepenbrock C, Berlin K,		
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01-SEP-2001; 2001WO-EP10074. 01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543. (EPIG-) EPIGENOMICS AG. Olek A, Piepenbrock C, Berlin K,	PD	07-MAR-2002.
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05-SEP-2000; 2000DE-1044543.  (EPIG-) EPIGENOMICS AG.  Olek A, Plepenbrock C, Berlin K,	PR	01-SEP-2000; 2000DE-1043826.
(EPIG-) EPIGENOMICS AG. Olek A, Piepenbrock C, Berlin K,	PR	05-SEP-2000; 2000DE-1044543.
Olek A, Piepenbrock C, Berlin K,	PΧ	(EDIG-) EDIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K,	XX	
	PI	Piepenbrock C, Berlin K,
	2 %	WDT 2002-371830 //0

Human ORF1796 cDNA

Claim 12;

56pp + Sequence Listing; 56pp; German. .

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RESULT 2
ABQ41021/c
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Best Local
Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
                                                                                                    Olek A,
                                                                      WPI; 2002-371829/40
                                                                                                                                       (EPIG-)
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05-SEP-2000;
                                                                                                                                                                                                                 01-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one
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                                                                                                                                                                                                                                                                                                                                               cell differentiation;
                                                                                                                                  EPIGENOMICS AG.
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22; Conservative
                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA;
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                                                                                                                                                                 2000DE-1043826.
2000DE-1044543
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78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.4;
Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                    rvous system; cardiovascular; single nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                                                    cytosine;
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CC Cytosine (C) but not methylated C, to uracil, then part or the yellowing (C) but not methylated C, to uracil, then part or the yellowing (C) but not methylated C, to uracil, then part or the yellowing (C) but that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one contains the provide of the yellowing contains the provide of the yellowing contains the cardior peptide-nucleic acid (PNA) oligomers and the degree of hybridised to the two classes of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue CC methylation status of many C residues to be determined simultaneously.

Annialio-AROSAI21 represent genomic DNA sequences used to illustrate the
                     Sequence 510 BP; 202 A; 151 C; 45 G; 112 T; 0 other;
                                                                                 ABQ13410 ABQ54121 represent genomic DNA sequences used to illustrate method for determining the degree of cytosine methylation described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining methylation of a particular cytosine in a motif 5'-CpG-genomic sample of DNA. The sample is treated chemically
                                                                       the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      es a novel method for determining the degree cular cytosine in a motif 5'-CpG-3', present The sample is treated chemically to convert ethylated C, to uracil, then part of the geno
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in
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Matches
                                           Best
                                                  Query Match
                                         Local
34
       1 CGTTCGTGGGATAGTCCGTCATGGTGTT 28
                                l Similarity
22; Conserv
                              65.7%;
ilarity 78.6%;
Conservative
                             ; Score 18.4; D; Pred. No. 43; 0; Mismatches
                                               DB
                                              24;
                          ,6
                                              Length
                             Indels
                                              510;
                            0;
                            Gaps
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밁 δ

CGTTCGTCGGATAGTGTGTTAGGTTGTT 7

RESULT 3
ABQ19830
ID ABQ1 drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; Oligonucleotide for detecting cytosine methylation SEQ ID 12-JUL-2002 (first entry) ABQ19830; ABQ19830 standard; DNA; 565 BP ŏ 6421.

Homo sapiens.

WO200218632-A2.

07-MAR-2002

01-SEP-2001; 2001WO-EP10074

01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543.

(EPIG-) EPIGENOMICS Ą

Olek Piepenbrock C, Berlin ζ, Guetig

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in for diagnosis and prognosis, comprises selective hamplicons from chemically treated DNA selective hybridization of. genomic DNA, useful

Claim 12; 56pp + Sequence Listing; 56pp; German

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                                                                                         Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                          Olek A,
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05-SEP-2000; 2000DE-1044543
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genomic sample of DNA. The sample is treated chemically to con
cytosine (C) but not methylated C, to uracil, then part of the
DNA that contains the target C is amplified to form a labeled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular;
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                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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78.6%;
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Pred. No. 4
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This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present genomic sample of DNA. The sample is treated chemically to convert

in

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins

is

Claim

1; SEQ ID NO 7073; 21pp + Sequence Listing; English.

Claim 12;

56pp + Sequence Listing; 56pp; German.

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RESULT 5
ABL04197/c
ID ABL04197 standard; cDNA;
XXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one comments of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method of contenting the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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                                                                                                                                    New isolated nucleic acid genes from Drosophila and interactions
                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                               23-MAR:2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 7073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytosine (C) but not methylated C, to uracil,
                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL04197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 565
                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                              (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the disclosure of the invention.
                                                                                                                                                                                                          2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 CGTTCGTCGGATAGTGTTAGGTTGTT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                           ABB60094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           gene;
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78.6%;
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                                                                                                                                                                                                                                    PWD,
                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No. 44;
                                                                                                                                                                                                                                    Myers; EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell signalling; insecticide;
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ABL04196/c
ID ABL041
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Best Local
                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes, for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                    sequences (ABL01840-
(ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                        Claim 1
                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide
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The sequence data for specification, but a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-656860/75
                                                                    Similarity
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CGTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                                   7330 BP;
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 7070; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
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                                                                                                            2139 A; 1620 C; 1570 G; 2001 T;
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                                                                 65.7%; Score 18.4; 78.6%; Pred. No. 6
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78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                       detection reagent for detecting for elucidating cell signalling
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Pred. No. 55;
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                                                Indels
                                                                                                              0 other;
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                                                                             Length 7330;
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0;
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RESULT 7
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                      05-MAR-1992;
                                                                                                          CDS
 05-MAR-1992;
                                          24 -SEP-1993.
                                                              JP05244959-A
                                                                                                                                      Saccharomyces
                                                                                                                                                        Urea amidolyase; URL; yeast;
                                                                                                                                                                             Urea amidolyase
                                                                                                                                                                                                    10-MAY-1994
                                                                                                                                                                                                                                            AAQ49460
                                                                                                                                                                                                                         AAQ49460;
                                                                                                                                                                                                                                                                                                2598
                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                             CGTTCGTGTGATAGTGCGAATTGTTGTT
                                                                                                                                                                                                  (first entry)
                                                                                                                                     cerevisiae.
92JP-0084531
                    92JP-0084531
                                                                                                    Location/Qualifiers 627..6134
                                                                                 /product= URL
                                                                                             /*tag=
                                                                                                                                                                                                                                           cdna;
                                                                                                                                                       recombinant plasmid; ss
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DNA having the genetic information of urea amidolyase originated from Saccharomyces yeast - can be used to prepare high purity urea amidolyase by culturing the transformant comprising the DNA Claim 1; Page 10-17; 17pp; Japanese.

WPI; 1993-338925/43. P-PSDB; AAR42839: (TOYM ) TOYOBO KK.

This sequence encodes a protein which has urea amidolyase (URL)-activity and is derived from yeast. This sequence may be used within a recombinant plasmid for the production of highly pure URL.

Sequence 6265 BP; 1873 A; 1156 C; 1361 G; 1875 T; 0 other;

Ş Query Match
Best Local Similarity
Matches 21; Conserv 1 CGTTCGTGGGATAGTCCGTCATGGTG Conservative 64.3%; 80.8%; 0; Score 18; DB Pred. No. 95; 0; Mismatches 26 14; 5; Length 6265 Indels 0

Gaps

0;

XXXX AAS59566 standard; DNA; 34088 8 밁

3683

CGTTCATGGGAAAGACCGTGATGATG 3708

13,-FEB-2002 (first entry)

AAS59566

Propionibacterium acnes immunogenic protein encoding DNA #61.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; inflammatory lesion; acne vul dermatological; osteopathic;

Propionibacterium acnes.

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WO200181581-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC Prophonibacterium acroes immunogenic polypeptides. The proteins and their cdiagnosis of medical conditions caused by P. acroes. The disorders include SAPHO syndrome (synovitis, acroe, pustulosis, hypertosis and content syndrome (synovitis, acroe, pustulosis, hypertosis and content syndrome (synovitis, acroe, pustulosis, hypertosis and content syndrome (synovitis, acroe, pustulosis, hypertosis and content syndrome (synovitis, acroe, pustulosis, hypertosis and content syndrome (synovitis, acroe, pustulosis, hypertosis and system, however it is particularly involved in the inflammatory lesions associated with acroe culgaris. A method for detecting the presence or absence of P. acroes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acroes proteins. These antibodies can be used to downregulate expression and activity of P. acroes polypeptides and therefore treat P. acroes infections. The antibodies may also be used as considered to treat P. acroes in a cristian. This sequence encodes the college shown in ANUS-556-ANUS-4928 and ANUS-756-ANUS-622.

CC Note: The sequence data for this patent did not form part of the printed content sequences and the electronic format directly from WIPO at firm who in formation is electronic format directly from WIPO at firm who in formation is electronic format directly from WIPO at firm who in formation is electronic format directly from WIPO at firm who in formation is according to the printed at the printed specific acroes presence in the printed at the printed specific acroes presence in the printed at the printed specific acroes presence in the printed at the printed specific acroes presence in the printed at the printed specific acroes presence in the printed specific acroes presence in the printed at the printed specific acroes presence in the printed at the printed speci
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Best Local S
Matches 20
                             Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; hematopoiesis regulation; themostaetic; hemostatic; haemostatic; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW, Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN76849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN76849 standard; cDNA; 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                         Human ORF1796 cDNA,
                                                                                                                                                                                                                                                                                                                                                                    08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L'maisonneuve J, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No 61; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6991 A;
                                                                                                                                                                                                                                                                                         SEQ ID NO:3591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11002 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9453 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 34088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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2 GTTCGTGGGATAGTCCGTCATGGTGTT 28

Matches Query Match Best Local 9

21;

Conservative

0

Mismatches No.

Indels, Length

Gaps

0

Similarity

62:18; 77.88;

Score 17.4; Pred. No. 1

.2e+02 DВ

24;

297; 0

Sequence

297

BP; 66

A; 99 C;

78 G;

54 T; 0 other

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cc and antiinfective activity, and may also be involved in the determination co of bodily characteristics, fertility and behaviour. ORFX proteins, curuleic acids and antibodies may be used in the treatment of cancers, cc other proliferative disorders such as psoriasis and benign tumours, careful disorders such as perial and benign tumours, concerning the concerning termination of cancers, disorders, disorders, disorders, disorders, disorders, disorders, disorders, concerning transplantation, disorders of tissue growth and regeneration, cc diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester concerning the party of the concerning transplantation. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous course. In genetic diagnosis, and in forensis biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity. Of ORFX concerning and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the concerning of the diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, and methods of screening individuals for a predisposition to offer associated disorder. The ORFX proteins of the invention have a wid range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopolesis regulation, cell differentiation, immune modulation, haematopolesis regulation, cell differentiation, immune modulation, haematopolesis regulation, clisue growth, angiogenesis, activin or inhibin activity, chemotactic chemokinetic activity, haemostactic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        designated ORF (open reading frame) 1-4534, and sequences ABN75054-BBN75587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatological; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue growth disorder; tissue regeneration hypothyroidism; cholesterol ester storage d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2000; 2000US-206690P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2001; 2001WO-US17076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190366-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiant; hypotensive; antithyroid; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vasotropic; antipsoriatic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-106200/14.
DB; ABP32823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2508pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rdorroou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes mellitus; fection; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS
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ABQ46568
ID ABQ4
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                                                                            RESULT 11
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                                                                                                                                                                                                                                              Query Match
Best Local
Matches 1
            ABQ46568
                                          ABQ46568
                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect mycobacterial nucleic acids (genomic DNA, CDNA or mRNA) in biological for detecting a given mycobacterium of interest. By aligning the polynucleotides contained in the recombinant BAC vectors it is possible
                                                                                                                                                                                                                                                                            are useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABQ62492 to ABB61228 and ABB81227 to ABB81230 represent sequences used in the
                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                      exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 70; 161pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation of polynucleotides from mycobacterial genomes, detection of Mycobacteria and for combating tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ62757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT | 1999. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis; Mycobacterium.bovis; mycobacterium; detection; BAC vector; bacterial artificial chromosome; tubercu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ627,57;
                                                                                                                                                                                                                                                                                                                     physically map a polynucleotide of mycobacterial origin in a
plogical sample. The methods and vectors from the present invention
a useful in providing information for combating tuberculosis. It is
                                                                                                                                                                                  18; Conser
                                        standard; DNA; 541
                                                                                                                 GTTCGTCGGATAGTCCGTC 235
                                                                                                                                              GTTCGTGGGATAGTCCGTC 20
                                                                                                                                                                                                                                       346 BP; 53 A; 96 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchrieser-Brosch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0060756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-IB00740.
                                                                                                                                                                                           62.18;
94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                    present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                     Score 17.4; DB 21,
Pred. No. 1.2e+02;
                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R, 'Gordon S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC vector clone Rv240SP6.
                                                                                                                                                                                                                                      125 G; 70 T;
                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                      2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billault
                                                                                                                                                                        Indels
                                                                                                                                                                                                   Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis
                                                                                                                                                                        0;
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
ABQ46569/c
ID ABQ465
XX
AC ABQ465
XX
DT 12-JUL
XX
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RESULT 12

ABQ46569 standard; DNA;

541

12-JUL-2002 ABQ46569;

(first.entry)

밁 δÃ

450

2 GTTCGTGGGATAGTCCGTCATGGTGTT 28

GTTCGTGGGTTCGGACGTCGCGGTGTT 476

Matches

21; Similarity

62.1%; ilarity 77.8%; Conservative

Score 17.4; DB 24; Pred. No. 1.3e+02; 0; Mismatches 6;

Length Indels

o,

Gaps

0

201 G; 197 T; 2 other;

Sequence 541 BP; 82 A; 59 C;

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PA XXX PI XXX PI XXX PI XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                       DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The metho is used: (1) for diagnosis and/or progness of classes of oligoners.
                                                                                                                                                                                                                                                                                                                                 methylation of a particular cytosine in a motif 5'-CpG-3 genomic sample of DNA. The sample is treated chemically cytosine (C) but not methylated C, to uracil, then part
                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-cpg-3', present
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; 56pp + Sequence Listing; 56pp;
                                                                                                                                                                                                                                                                                                                  cytosine (C) but not methylated C, DNA that contains the target C is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amplicons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in for diagnosis and prognosis, comprises selective h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2001; 2001WO-EP10074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200218632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for detecting cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from chemically treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guetig
                                                                                                                                                                                                                                                                                                                                                                                                                                  German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n genomic DNA, useful hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular;
                                                                                                                                                                                                                                                                                                                             y to convert of the
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                                                                                                                                                                                                             The method
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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; Oligonucleotide for detecting cytosine methylation SEQ ID NO 33160.

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RESULT 13
ABN24612
ID ABN24
XX ABN24
XX ABN24
XX ABN24
XX Human
XX Human
XX Human
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Best Local :
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (pNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, quastrointestinal and recriments.
                                                                                                                                                                                                                                                                                                                                                                                                               of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for determining tmethylation of a particular cytosine in a motif 5' CpG-3' genomic sample of DNA. The sample is treated chemically t cytosine (C) but not methylated C, to uracil, then part of the cytosine (C) but not methylated C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA
                                     Human ORFX polynucleotide sequence SEQ ID NO:17701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug; side effect; cancer; central nervous system; gastrointestinal; respiratory system; single nucleo
Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                          24 -JUN-2002
                                                                                                           ABN24612
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 541 BP; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-371829/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2001; 2001WO-EP10074
                                                                                                                                               ABN24612 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200218632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell differentiation;
                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                          GTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                                                                                                                                                    GTTCGTGGGTTCGGACGTCGCGGTGTT
                                                                        (first entry)
                                                                                                                                             CDNA; 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            గ్ర
                                                                                                                                                                                                                                                                                                                        62.1%;
                                                                                                                                                                                                                                                                                                                                                                              A; 201 C; 59 G; 82 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K,
                                                                                                                                                                                                                                                                                                       Score 17.4;
Pred: No. 1.
0; Mismatche
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guetig
                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                         Length 541;
                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the degree
                                                                                                                                                                                                                                                                                                         0;
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic
                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 14
AAF63738
ID AAF63
XX

AAF63738

standard;

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344

CGTTCGTGATATGGTCCGCCAGGGTCT 370 CGTTCGTGGGATAGTCCGTCATGGTGT 27 Query Match Best Local S Matches 21

Similarity

62.1%;

Score-17.4; Pred. No. 1 Mismatches

6,

0;

Gaps

0

Length Indels

654;

Sequence 654 BP; 90 A; 194 C; 180 G; 190 T; 0 other;

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transplantation, considered in transplantation, hypothyroidism, considered in fectious storage disease, various immune deficiencies and disorders, infectious disease, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host arthritis, autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ireating or preventing a pathology associated with an ORRX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for preventing and treating cardiovascular disease, neurodec hyperproliferative disorders and autoimmune disorders
                                                                    N.B. The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                              reperfusion injury in various tissues and conditions resulting systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000US-206132P
29-AUG-2000; 2000US-228716P
                                                                                                                                                                                                                                                                                                     bone degenerative disorders, or periodontal disease, and i protection or regeneration and treatment of lung or liver
                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating burns, incisions, ulcers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention description, OREX, where X is 1-11491 (see rapid the factor). ABM15762 to ABM27252 encode the human OREX in the specification). ABM15762 to ABM27252 encode the human OREX proteins are useful for proteins given in ABP00010 to ABP11500. OREX proteins are useful for proteins given in ABP00010 to ABP11500. OREX proteins are useful for proteins given in ABP00010 to ABP11500. OREX associated with an OREX associated with an OREX associated with an OREX associated with a contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of the contraction of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106308/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200192523-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-2001; 2001WO-US10836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyperproliferative
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ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes substantially purified human ferred to as open reading frame, ORFX, where X is 1-11491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorder; psoriasis; benign tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative,
                                                              part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thyroiditis;
                                                                                                                                                                                                                                                                                                                 fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used in the
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03-APR 2001 (first entry)

AAF63738;

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RESULT 15
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ID ABL27
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                   Drosophila melanogaster.
                                                                          pharmaceutical; gene;
WO200171042-A2.
                                                                                        Drosophila; developmental biology;
                                                                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 33910.
                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                      ABL2747
                                                                                                                                                                                                                                                         ABL27479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein sequences may be used for the identification of compounds, e.g. pheromones and other semiochemicals, which may be used for pest management. The DNA sequences may also be used for behavioural studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulating the expression of the DNA encoding the receptors. The DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to polynucleotide sequences AAF63732 - AAF63777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         involving gustatory systems in various organisms. Also, the DNA sequence and also be used to track down gustatory receptor genes in insects that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid molecule Receptor protein useful for e.g. ic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which encode Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-061873/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-1999; 99US-0138668.
10-FEB-2000; 2000US-0181704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gustatory receptor; fruit fly; taste; crop damage; pest control; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200077208-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila gustatory receptor GR23A.1a DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for pest management -
                                                                                                                                                                                                                                                                                                                                               GTTCGTGGGAAACTCCGTGCTGGGATT
                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1149 BP; 255 A; 276 C; 292 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PJ, Clyne PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                      GTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 95-97; 227pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB75193
                                                                                                                                                                                                                                                                                                                                                                                                                              62.1%;
ilarity 77.8%;
Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prosophila gustatory receptor proteins represented by NB75193 - AAB75238. The invention includes methods for gustatory receptor ligands. Also included is a method for
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                     DNA; 1755 BP.
                                                                            ds.
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Pred. No. 1.
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                                                                                    cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 T; 0 other;
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Best Local Similarity
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                                                                                                                                                            discloses genomic DNA sequences (ABL16176-ABL30511), esequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 33910; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and interactions -
                                                                            Sequence 1755 BP;
                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                     useful in developmental biology and in ecell-cell interactions in higher
                                                                                                                                                                                                                                                                                            The invention relates
                                                                                                                                                                                                                                                                             capable of detecting 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                         Japable of detecting 1000 or more genes from Drosophila. The invention iseful in developmental biology and in elucidating cell signalling and sell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention listicides genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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       21;
       .Conservative
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                                                                386 A; 425 C; 437 G; 507 T; 0 other;
                      62.1%;
77.8%;
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Score 17.4; E
Pred. No. 1.5e
0; Mismatches
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                                      DB 23;
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Search completed: July 10, 2003, 19:52:53 Job time: 67.0831 secs

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Listing first 45 summaries
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1: /cgn2_6/ptodata/
  cgttcgtgggatagtccgtcatggtgtt
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-07-961-522-1
US-08-217-438-1
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US-08-321-978-1
US-08-321-978-1
US-08-321-978-1
US-09-342-681C-116
US-09-342-681C-116
US-09-342-681C-116
US-09-342-681C-724
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US-08-96-155A-724
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US-08-970-428A-13
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US-08-970-428A-13
PCT-US91-02994-1
US-08-970-428A-13
US-08-970-428A-13
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US-08-970-428A-13
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US-08-970-428A-13
US-08-970-428A-13
US-08-98-98-98-11
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US-09-060-756-256
4 US-09-103-840A-2
4 US-09-103-840A-1
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US-09-221-017B-876/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87 Patent No.
                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                       TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998
                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pair
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSS, Bruce
TITLE OF INVENTION: P.
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                        TELEFAX:
                                                                                TELEPHONE: 650 U. TELEPHONE: 650-494-0792
                                                                                                                              NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                              FILING DATE:
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/ENTION: P. GINGIVALIS
EQUENCES: 1120
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US-08-687-597-268
US-08-955-762-41
US-09-295-028-41
US-09-106-582-41
US-08-403-545-1
US-08-404-381-1
US-08-404-381-1
US-08-404-381-2
US-08-405-562-2
US-08-450-562-2
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US-08-984-709A-25
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            FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                    -09-103-840A-2
                                                                                         APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Mate
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OTHER INFORMATION: applicants are uncertain of ba
-09-060-756-256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ
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                                                                                                                                                                   PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Billault, Alain
ITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BACTLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF
ID NO
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Best Local Similarity 77.8%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 1, Applic
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
 SUPTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no /~~
FILING DATE: ^~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                          quence 1, Applic
tent No. 5874243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TILE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                      CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                      PPLICANT: Macina, Robert PPLICANT: Sathe, Ganesh
                                                                                                                                                                                                                                                                                                                                                                                                                                     3850511 CGTCGGTGGCGTTGTCCGGCATGGTGT 3850537
                                                                                                                                                                                                                                                           UMBER OF SEQUENCES: .
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                                                                                                                                                                         STREET: //y security: King of Prussia
                                                                                                                                                                                                                                                                         TLE OF INVENTION:
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                            19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGTTCGTGGGATAGTCCGTCATGGTGT 27
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                                                                                                                                                                                                                                                                                                                                                        Application US/08827291A
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                                                                                                                                                                                                       E: SmithKline Beecham Corporation
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHITE, Owen R.
אבסביג: US/08/827,291A
28-MAR-1997
                                                                                                           Diskette
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                                                                                                                                                                                                                                                                                                        Roberto
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Pred. No. 4
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Pred. No. 47;
0; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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Query Match Best Local Similarity Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                             TELEFAX: (415) 327-3231 (INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2696 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                               OUTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION UNMEER: 30,954
REFERENCE/DOCKET NUMBER: GF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5015
 OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
             TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                           NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: PALO ALTO
                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 635 BRYANT STREET
                                                           2696 base pairs
                                                                                                            (415) 617-8999
(415) 327-200
                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSSI-CAMPOS, AMALIA
JENTION: VACCINES FOR ACTINOBACILLUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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DNA (genomic)
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                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                       US/07/961,522
                                                                                                                                                                           33,208
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Pred. No.
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RESULT 8 US-08-321-978-1

Sequence 1, Application US/08321978 Patent No. 5801018

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                                                                              Query Match
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                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                   FEATURE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEIMONIAE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                  Local
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 60.7%;
Local Similarity 80.0%;
                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                         LOCATION:
                                                                                                                                                              TOPOLOGY: · linear
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2267 TTCGTGGGGTAGATCGTAATCGTGT 2291
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                           3 TTCGTGGGATAGTCCGTCATGGTGT 27
                                                     20;
                                                                  Similarity
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California
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                                                     Conservative
                                                                                                                                                                                                                                                            415-327-323
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Willson, Philp J
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                                                                 60.7%;
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                                                                  Score 17;
Pred. No.
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INFORMATION:

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Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROB
STREET: 285 HAMILTON AVE.
                                                                                                                                                                                                                                                               ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 327-32
NFORMATION FOR SEQ ID NO:
                                                                                                                                             PPLICANT: ROSSI-CAMPOS, AMALIA
ITLE OF INVENTION: VACCINES FOR ACTINOBACILLUS
ITLE OF INVENTION: PLEUROPNEUMONIAE
                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 90
PELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/321,978
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                Application US/08710584
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                                    9430
                                                                            PALO ALTO
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                                          CALIFORNIA
UNITED STATES OF
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Y: UNITED STATES OF AMERICA
                                                                                                                                         SEQUENCES:
                                                                                                                                                                                               GERLACH, GERALD WILLSON, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: ROBERTA L. ROBINS
285 HAMILTON AVE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2696 base pairs
                                                                                                                                                                                                                               POTTER, ANDREW A
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333..1973
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                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
                                                                                  AVE, SUITE 200
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Pred., No.
                                            AMERICA
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. 36;
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US-09-388-743-25
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US-09-388-743-25
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                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.7%;
Best Local Similarity 80.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09388743
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/388,743
CURRENT FILING DATE: 1999-09-02
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Singletary, George
APPLICANT: Zhou, Lan
TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
TITLE OF INVENTION: Use in the Production of New Starches
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 1144
                                                                                                                                                                                                     ORGANISM: Typha latifolia
                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        YPE: DNA
                                                                                                                                                                                                                                        ENGTH: 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US (FILING DATE: 12-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 333..1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2696 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
2267 TTCGTGGGGTAGATCGTAATCGTGT 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TTCGTGGGATAGTCCGTCATGGTGT 27
                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                    60.0%;
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                                                                   0; Mismatches
                                                                                    Score 16.8;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB
Pred. No. 36;
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                                                                                                   DB
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                                                                                                Length 2418;
                                                                   Indels
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                                                               Gaps
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RESULT 11 US-09-342-681C-116/c ; Sequence 116, Application US/09342681C

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RESULT 13
US-09-221-017B-147
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Sequence 18, Application US/09342681C
                                                                                                                                                                                       Query Match
Best Local Similarity
Thes 21; Conserve
                                                             Sequence 147, Application US/09221017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n is a, c, t or g 09-342-681C-116
                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/342,681C CURRENT FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 1998-12-1 NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/092,279
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/342,681C CURRENT FILING DATE: .1999-06-29
                                                                                                                                                                                                                                                                     09-342-681C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/112,366
                                                                                                                                                                                                                                                                                                                                                                                                        RIOR FILING DATE: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                             tent No. 64447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT:
                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (43)
                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           OFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
ILE REFERENCE: 52978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins ILE REFERENCE: 52978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JAME/KEY: misc_feature
JOCATION: (528)..(2756)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                 YPE: DNA
                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              ID NO 18
PPLICANT: ROSS, Bruce C.
ITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/092,279
                                                                                                                                          3466 CGTTGGTGGGAAATTGCTTGTTGGTGTT 3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2010 CGTTGGTGGGAAATTGCTTGTTGGTGTT 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                       1 CGTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                                                                                                                                                                                                                                                                                4235
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                                                                                                                                                                                                                                                                                (433)..(1779)
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                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                    60.0%;
75.0%;
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75.0%;
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                                                                                                                                                                                                                    Score 16.8;
Pred. No. 48;
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Pred. No. 45
                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
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                                                                                                                                                                                                                                   Length 4235;
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                                                                                                                                          US-08-936-165A-217
                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                   Matches
                                                                                          ENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                               APPLICANT:
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                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-813-5600
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                              APPLICANT
                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                       NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1...5476
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PP2911 FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5476 base pairs
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                                                                                                                                                                                                                                                                  Conservative
Nicholas, Richard
              Knowles, David
Lonetto, Michael
                                                          Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: Windows FastSEQ for Windows Version
                                             Hodgson, John
                                                                            3lack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                          PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORRISON & FOERSTER
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10-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gladys
                                                                            Michael
                                                                                                                                                                                                                                                                               60.0%;
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ER: 27340-20021.00
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5013 CATTCGGTGGAGAGCCCGGCATGGTGAT 5040
                                                                                                                1 CGTTCGTGGGATAGTCCGTCATGGTGTT 28
17, Application US/08936165A 6348582
                                                                                                                                                            Mismatches
                                                                                                                                                            Indels
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Score 16.8; Pred. No. 5

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Length 5476;

<u>.</u>

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FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                              RESULT:15
US-09-134-001C-724/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84...
Thes [19; Conservative
LENGTH: 948
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
-09-134-001C-724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
MOLECULE TYPE:
-08-936-165A-217
                                                                                                                                                                                                                                                                                                            equence 72
                                                                                                                                                                                                                         PPLICANT: Lynn Doucette-Stamm et al ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS ITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/936,165
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME Gimmi, Edward R
NAME Gimmi, Seward R
                                                                                                                                                                                                                                                                                                NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS:
OPERATING SYSTEM: DOS:
SOFTWARE: FASTSEQ for Windows Version 2.0
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              724, Application US/09134001C . 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King of Prussia
E: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTGGGATAGTCCGTCATGGTG 26
                                                                                                                                                                                                                                                                                                                                                                                                                TCTTGGGATACTCCGTTAGGGTG 273
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Reichard, Richard
Rosenberg, Martin
Ward, Judith
VENTION: No. 6348582el Prokaryotic Polynucleotides,
VENTION: Polypeptides and Their Uses
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Query Match 59.3%; Score 16.6; DB 4; Length 948; Best Local Similarity 82.6%; Pred. No. 47; Matches 19; Conservative 0; Mismatches 4; Indels 0;
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Gaps

Search completed: July 10, 2003, 20:28:02 Job time: 33.5213 secs

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Title:
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Match
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US-09-796-692-4625

US-09-796-692-4625

US-10-156-761-101

0 US-09-826-508-23

0 US-09-815-242-7956

0 US-09-918-909-23

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                                 Sequence 1, Appli
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Sequence 3874, Ap
Sequence 33, Appl
Sequence 4625, Ap
Sequence 4625, Ap
Sequence 1019, Appl
Sequence 23, Appl
Sequence 7956, Ap
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Sequence 1,
Sequence 1
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#### ALIGNMENTS

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US-10-087-631B-12/c

; Sequence 12, Application US/10087631B
; Publication to. US20030054372A1
; GENERAL INFORMATION:
APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMIN
; TITLE OF INVENTION: CONTROL
; TITLE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 28
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-087-631B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/087,631B CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING TITLE OF INVENTION: CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JAEGER, STEPHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: complement to ST778
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 9;
Pred. No. 0.00087;
); Mismatches 0;
                                                                                      THE DETERMINATION OF A NUCLEIC ACID USING
                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                  Sequence 6429, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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                                 CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2002-03-01
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                                                                                                                                                                                                                                   APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-087-631в-11
                                                                                                                                                                                                             PPLICANT
                                                                                                            PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
ILE REFERENCE: 249-262
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ITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
ITLE OF INVENTION: CONTROL
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                                                                                                                                                                    SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                                                                                                                                                                           ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                   , SATOSHI
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of HCV type 1 genome
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RESULT 6
US-10-156-761-5471
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; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
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US-10-156-761-6429
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                        Sequence 5471, Application US/10156761 Publication No. US20030119018A1
                                                                                                 APPLICANT: SHIBA, TADAYOSHI
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                                       APPLICANT: HATTORI, MASAHIRA
FITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                     APPLICANT:
                                                                                                                   APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                      APPLICANT: OMURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/156,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URRENT FILING DATE: 2002-05-29
RIOR APPLICATION NUMBER: JP 2001-204089
RIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: RIOR FILING DATE: 2001-0
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APPLICATION NUMBER: US/10/156,761 FILING DATE: 2002-05-29
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23; Conservative
                                                                               SAKAKI, YOSHIYUKI
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
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8-02
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Pred. No.
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; LOCATION: (1)..(1572)
US-10-156-761-5471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 5471
LENGTH: 1572
TYPE: DNA
                                                                                      Query Match
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Best Local Similarity
                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                          TELEFAX: (301) 309-8512
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-781-986A-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 5, Application US/08781986A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lication No. US20030054436A1
NERAL INFORMATION:
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                NAME: Bensum, 30,446
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB
FELECOMMUNICATION INFORMATION:
(301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette,
                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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6487 GTTCATAGGCTAGTTCGTAATAGTGTT. 6461
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                                                          Similarity
21; Conserv
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                                                                                                                                                 nucleic acid
EDNESS: double
                 GTTCGTGGGATAGTCCGTCATGGTGTT 28
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9410 Key West Avenue
                                                                                                                                                                            8549 base pairs
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                                                            Conservative
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                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus Polynucleotides and Sequences 5255
                                                                        62.18;
77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                       PB248PP
                                                                       Score 17.4;
Pred. No. 1.
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Pred. No. 99;
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                                                        Mismatches
                                                                        .1e+02;
                                                                                      DB 7;
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                                                                                     Length 8549;
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US-10-156-761-1/c
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Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10156761 Publication No. US20030119018A1
SEQ ID NO
                                                              APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI
                                  PRIOR FILING DATE:
                                                PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                                                                                                                         APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                 513413 GTTCCTGGGTGTGTCTGTGATGGTGTT 513439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                          INFORMATION:
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                SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                   SAKAKI, YOSHIYUKI
                                                                                                                                                                                                     SHIBA, TADAYOSHI
                                                                                                                                                                                                                      ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                        IKEDA, HARUO
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Koop, Ben F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (206) 622-4900
                 NOS:
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77.8%;
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Pred. No. 1
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NAME/KEY: misc_feature; LOCATION: (4187715); OTHER INFORMATION: a, t, US:10-156-761-1
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                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Genbank 09-880-107-3874
                                                                                                    PPLICAN1
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                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URRENT APPLICATION NUMBER: US, URRENT FILING DATE: 2001-06-1
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                                                                                                                                                                               FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                      Similarity
19; Conserv
                                                   Wang, Jian-Rui
Zhao, Qing A.;
Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn
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Wang, Zhiwei
Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                            Ma, Yunqing
                                                                                                                                      Liu, Chenghua
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCGTGGGATAGTCCGTCATGGTGTT 28
                                                                                                           hou,
                                                                                                                                                                                                           Application
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Gene Logic, Inc
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                       Chongjun
                                                                                                                                                                                            US20020197679A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09880107
020142981A1
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                                                                                                           Ping
                                                                                                                                                                  Tom
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86.48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                            Accession No. US20020142981A1 Z29481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             us/09/880,107
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                                                                                                                                                                                                                                                                                                                                             Score 17.2;
Pred. No. 1
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Pred. No. 1
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                    APPLICATION NUMBER: 60/223,378
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APPLICATION NUMBER: 60/222,903 FILING DATE: 2000-08-03 APPLICATION NUMBER: 60/223,416

DATE: 2000-08-04

APPLICATION NUMBER: 60/218,950

2000-07-14

PLICATION NUMBER: 607 LING DATE: 2000-05-22

60/206,201

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RESULT 12
US-09-796-692-4625/c
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; LOCATION: (103)..(963)
US-10-098-841-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 86. Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: pt
                                                                                                                                                                                                CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/796,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/598,042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIOR FILING DATE: 2000-06-20
RIOR APPLICATION NUMBER: 09/552,317
RIOR FILING DATE: 2000-04-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TGTGATAGTCCTTCCTGGTGTT 223
                                                            PLICATION NUMBER: 60/200,779
LING DATE: 2000-04-28
                                                                                                                                                                                                                                                           f: Mannion, Jane
INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
INVENTION: HEMATOLOGICAL MALIGNANCIES
                                                                                                                                                                LICATION NUMBER: 60/190,479
                                                                                                                                                                                                                                                                                                                                                    1: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1320
                                          CATION NUMBER: 60/200,999
        CATION NUMBER: 60/202,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pt_FL_genes Version 1.0
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                                                                                                                                            ATION NUMBER: 60/200,545
                                                                                                              ATION NUMBER: 60/200,303
                                                                                                                                                                                                                                                                                                                                ligate, Paul A.
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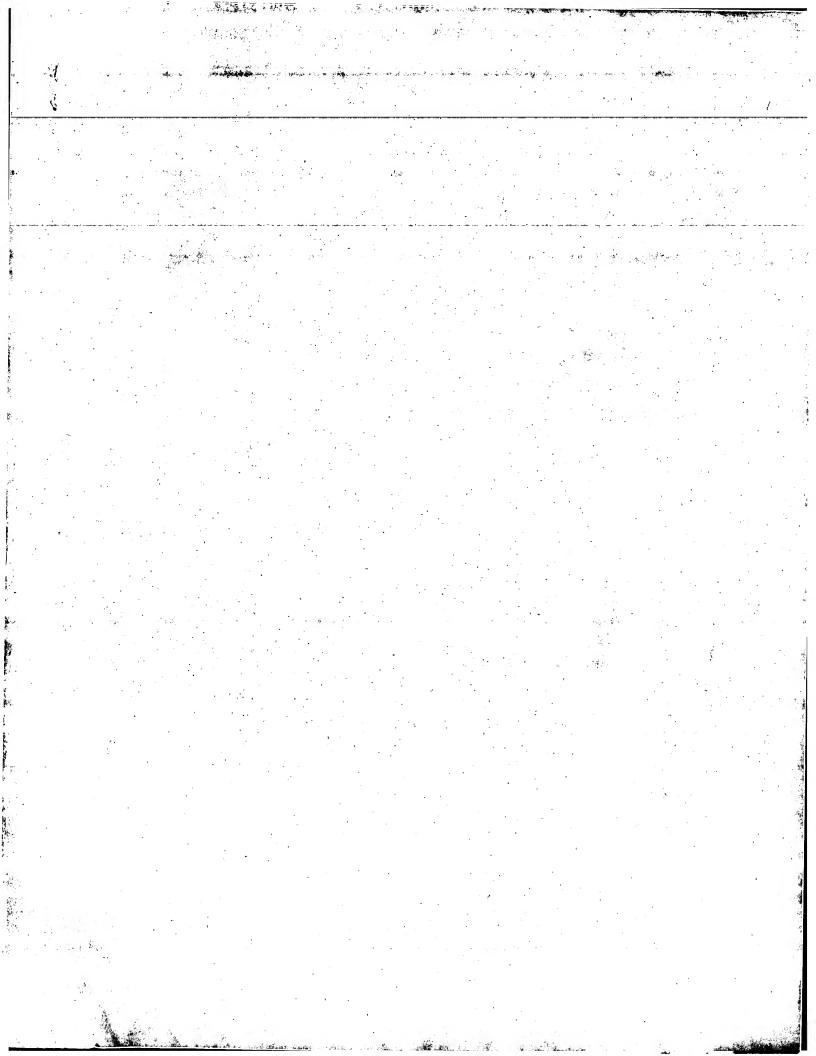
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; TYPE: DNA .
; ORGANISM: Homo sapiens
US-09-796-692-4625
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US-10-040-862-4625
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SOFTWARE: FastSEQ for Windows Version 3.0
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blication No. US20030078396A1
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                                                                                                                                                                        ENGTH: 493
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/223,378
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DATE: 2000-08-03
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LENGTH: 924
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CURRENT FILING DATE: 2001-04-05
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CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                            TITLE OF INVENTION: and POINT TILE REFERENCE: GP-70744USB
                                                                                                                                                                                                                                                                                          ITILE OF INVENTION: G Protein-Coupled Receptor Polypeptides
ITILE OF INVENTION: and Polynucleotides
                                                                                                                                                                                                                                                                                                                              APPLICANT: Nabil Elshourbagy
APPLICANT: Lisa Vawter
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LOCATION: (1).
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ORGANISM: HOMO SAPIENS
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	V05875	5024176	5017850	Pan tro	AGENCOU	5025082	OGBN LSC	OGBNESC	SD17903	QGG20P15.	QGF14L0	Լ01251.	040717.	SD26015	RE27348.	RE56658.	RE02892.	RE083	1 pep004	os75b11.	)GG14A13	ž	JI-R-BT1	56006	3B348944	947049B	347049C	C3-HTO	Ö	IS 5503	1-01CH	CH230-5	5023905	RPCI-23	CH230-5	LM0162E	HS_5310_	CH230-1	RPCI11-1	

### ALIGNMENTS

RH18118.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH18118 5 similar to sqd: rBan0017791 GO:[RNA binding (GO:0003723); RNA binding (GO:0003723)] located on: 3R 87F7-87F7;: 08/17/2001, mRNA sequence. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. BDGP/HHMI RH Drosophila Unpublished (2001) Contact: Stapleton, M. Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 ,R., Gonzālez,M., Guarin,H., Harri Mungall,C.J., Nunoo,J., Pacleb,J., Phouanenavong,S., Wan,K., Yu,C., Le 1 (bases 1 to 475)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., BI611725.1 BI611725 BI611725 StapLeton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., Georg fruit fly: GI:15507250 EST Project 475 bp Yu, C., Lewis, S.E., Harris,N., Li,P., Liao,G., Misra,S., eb,J., Paragas,V., Park,S., linear Celniker, S. and Rubin EST 07-SEP-2001

Email: http://www.fruitfly.org/EST/ hit genomic AE003701: arm:3R [9357]

[9357746,9566163]

est@fruitfly.berkeley.edu

Plate: RH.181 row: B column: 6 High quality sequence stop: 291. estimated-cyto:87F4-87F14: 08/17, Plate: RH.181 row: B

on/Qualifiers

FEATURES

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VERSION
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AZ567844
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                  BM597959
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                                                                                                                                                                      Similarity
                                                                                 CGTTCGTGGGAGCGGCCGTGATGGTCT 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dept. of Pathobiology, College of Veterinary Medicine University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malaria parasite P. vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ567844 590 bp
239PvH07 Pv MBN #30 Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ail: damej@mail.vetmed.ufl.edu
                                                                                                                                                                                                                                    142 a
                                                                                                                                                    67.9%;
llarity 81.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: M13(-20) forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                              Host leukcytes were extracted from P. vivax infected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) acid washed 0.1 mm plass beads, then through a Plasmodipur Whatman (ETI) powder (1.2 ratio volume of blood to CFI1), and finally centrifuged through a 50% percoll density
                                                                                                                                                                                                                                                     SK(+), and E. coli XL-10 Gold
                                                                                                                                                                                                                                                                                      cushion. Purified DNA was digested with mung bean nuclease in the presence of 44% formamide at 500C as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). Digested DNA was blunt-ended using T4 DNA Polymerase and size fractionated
                                                                                                                                                                                                                             ligation mixture.
138 c 155
                                                                                                                                                                                                                                                                    Over a Sepharose CL-2B column. F 500bp-4kb were ligated into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript SK(+) vector DNA,
excised from lambda ZAP; Site_1: EcoR V; Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'dev_stage="asexual blood forms"
'lab_host="Saimiri boliviensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:5855"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Plasmodium vivax"
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                                                                                                                                             Score 19; DB
Pred. No. 4.5e
0; Mismatches
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vivax genomic 3', DNA sequence.
                                                                                                                                                                                                                                                 transformed with the
                                                                                                                                                                        Length 590;
                                                                                                                                                                                                                                                           ractions in the size range
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EST 25-FEB-2002
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REFERENCE AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 406)

Craniata; Vertebrata; ¡Catarrhini; Hominidae;

Euteleostomi;

RESULT 2 AV732708

47 CCTTCTTGGGATAGACCTTCATGCTGTT 320

1 CGTTCGTGGGATAGTCCGTCATGGTGTT 28

BASE COUNT

150 a

/lab\_host="DH5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site\_1: XhoI; Site\_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
cre recombinase. Plasmid cDNA library."

/clone\_lib="RH Drosophila melanogaster normalized Head

'sex="male and female"
'dev\_stage="Adult"

/organism="Drosophila melanogaster" /db\_xref="taxon:7227" /clone="RH18118"

Query Match
Best Local S
Matches 23

Similarity 23; Conser

Conservative

0;

Mismatches

Score 20; Pred. No.

DB 13; 1.5e+02; 5;

Length 475;

0;

Gaps

0

DEFINITION ERSION -

AV732708 AV732708 HTF Homo sapiens AV732708

406 bp mRNA linear EST 17-OCT-2 cDNA clone HTFBCH01 5', mRNA sequence.

EST 17-OCT-2000

ocus CCESSION

EYWORDS

AV732708.1

ORGANISM

COMMENT

Homo sapiens cDNA HTF clones Unpublished (2000)

(Jases 1 to \*vo, u,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H. i,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zer S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,

, Xiao,H., Xu,X., u,Z., Zeng,L., Xu , Lu,G., Hu,R.,

W., Tu,Y., Jia,J., Fu,G., Chen,Z. and Han,Z.

Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China

01203, P. R. China el: 86-21-50801919(ex.45)

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BASE COUNT
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                     Query Match
Best Local
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. /
                                                                                                                                                                                                This clone
                  milarity
                                                               153
                                                                                                                                                                           hanzg@chgc.sh.cn
lone is available at CHGC in Shanghai.
Location/Qualifiers
                                                               þ
                                                                                'note="Vector:
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTFBCH01"
                                                                                                      /tissue_type="Hypothalamus"
/dev_stage="Adult"
                  67.9%;
81.5%;
                                                             50 c
              Score
Pred.
                                                        65 g
                                                                     pBluescript sk(-); Site_1: EcoRI; Site_2:
            19; DB 10;
No. 3.9e+02;
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                   Length 406
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RESULT 5
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                                                                                                                                                                 Gossypium hirsutum.

Gossypium hirsutum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eu

Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                   AI055301 667 bp mRNA linear | coau0003J18 Cotton Boll Abscission Zone cDNA Library hirsutum cDNA clone coau0003J18 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 w. Gude Dr., Rockville, Tel: 2404533151 Fax: 2404534580
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: HoltRA@celera.com Plate: NU010049UU row: C Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17000687506516 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449733180 5', mRNA sequence.
                                                                                                                                                                                                                                                                 EST
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                                                        Contact: Wing RA
                                                                          Unpublished (1998)
                                                                                         Wan, C.-H., Yu, Y., Sasinowski, M. and Wing, R.A. Cotton EST Database: Sequence Analysis of 200 Abscission Zone Library
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                                                                                                                                                (bases 1 to 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference Reagent Resource Center (www.malaria.mr4.org)" 185 c 186 g 135 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lone_lib="A.Gam.ad.cDNA.blood1"
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Pred. No.
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Hoffman, S.L.
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                                                                                                             cDNA Clones from
                                                                                                                                                                                       eudicots;
                                                                                                                                                                                                                                                                                                                                                          EST 16-JUL-1998
                                                                                                                                                                                                    Tracheophyta;
                                                                                                                                                                                                                                                                                                                                       Gossypium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing,R., Close,T.J., Kleinhofs,A., Wise,R.,

Wing,R., Close,T.J., Kleinhofs,A., Wise,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVSMEC0019C13f Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
On Dec 18, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVCDNA0003 (Etiolated HVSMEC0019C13f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
Total hq bases = 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chói,D.W., Fenton,R.D., Oates,R. and Main,D.
Greylopment of a genetically and physically anchored EST resource bevelopment of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                          lemson University
00 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTCGTGGGATTGTTCTTCCTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticeae; Hordeum.
                                                                                                                                                                                                                                           primer: AATTAACCCTCACTAAAGGG
h quality sequence stop: 671.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer:
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864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: SP030 (AACAGCTATGACCATGATTA)
quality sequence stop: 325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     864 656 7288
864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stratagene (U.S.A.: #837201."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is a Uni-ZAP XR custom cDNA library made by Stratagene (U.S.A.: 1-800-424-5444): Stratagene
/note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /GLONE_ILD- VCLORE, // (Alb_host-"XLI-Blue MRF'"
// Alb_host-"XLI-Blue MRF'"
// note-"Vector: Uni-ZAP XR; Site_1: EcoRI;
// note-"Vector: Uni-ZAP XR custom cDNA library n
                                                                                                   /clone_lib="Hordeum vulgare seedling
HVcDNA0003 (Etiolated and unstressed)
                                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="coau0003J18"
/clone_lib="Cotton Boll Abscission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon
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                                                                              tissue_type="Seedling shoot"
                                                                                                                                            clone="HVSMEc0019C13f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism-"Gossypium hirsutum"
                                                         lab_host="TJC121"
                                                                                                                                                                 db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:13109301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this sequence version
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
. 4.7e+02;
5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replaced gi:11883972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Begum, D., Frisch, D., Yu
,J., Choi, D.W., Fenton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zone
                                                                                                            shoot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Site_2: XhoI;
                                                                                                                       EST library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Other_GSSs: RPCI11-110C18.TV
                                                                                           ttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
eq primer: Sp6
                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao, William Ni
Department of Eukaryotic Genomics
                                                                                                                                ACPAC Resources (http://bacpac.med.bu
esearch Genetics (info@resgen.com). B
                                                                                       ass: BAC ends
                                                                                                                                                      brary availability, please contact Pieter de Jong
Leter@deJong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                      hao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPCI11-110C18.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ammalia; Eutheria; (bases 1 to 521)
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                                                                                                                                                                                                                                              12 Medical Center
1: 301 838 0200
x: 301 838 0208
                                                                                                                                                                                                              ones are derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                  Institute
                                                                                                                                                                                                                                                                                                                                                                                                 of BAC End Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
              /organism="Homo sapiens"
/db_xref="GDB:7541921"
                                                                 Location/Qualifiers
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http:/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of
                                                                                                                                                                                                                                                                            Center Dr.,
                                                                                                                                                                                                                                                                                                                                                                     (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cked at the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ose laboratory at the University of Calif-
verside (Choi, Close, Fenton). Phagemids
                                                                                                                                                                                                                                                                        for Genomic Research
Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ified one primary unamplified cDNA library was made, I million pfu were in vivo excised to give pBluescript DNA phagemids. These steps were performed in the TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //www.genome.clemson.edu/projects/barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
/ c 284 g 219 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPCI-11
                                                                                                                                                                                            from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                    ., Nierman, W., Malek, J., de Jong, P. and Venter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                     Nierman, Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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                                                                                                                                       iffalo.edu/ordering) or from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               near GSS 07-MAY-1999 clone RPCI-11-110C18,
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                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
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BH282580/c
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                          source
       Similarity
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RESULT 7 AQ350115/c

BASE COUNT

Query Match

Loca.

REFERENCE

AUTHORS

ACCESSION VERSION VERSION SOURCE

ORGANISM

FEATURES

source

Conservative

66.4%;

Score 18.6; DB 17; Pred. No. 6.6e+02; 0; Mismatches 4;

Length 549;

0;

Gaps

0

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Query Match
                                                                                                                                                                                                                                    Class: BAC ends
                                                                                                                                                                                                                                                                       page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 128 row: I column a
                                                                                                                                                                                                                                                                                      (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm) page: http://www.tiaro.com/pacpac/or ering_information.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat BAC End Sequences from Library
Unpublished (1999)
Other_GSSs: CH230-12818.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 bp
CH230-12818.TJ CHORI-230 Segment
CH230-12818, DNA sequence
BH282580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao,S., Shetty,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                           rrtment of Eukaryotic Genomics
Institute for Genomic Research
Medical Center Dr., Rockville,
301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Shetty, J., Shatsman, S., Tsegaye, G., Gebregeorgis, E., Overton, L., Russell, D., P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                         szhao@tigr.org
          CHORI-230
Pieter de
a 111 c
                                /cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library
                                                                                                                        /db_xref="taxon:10116"
/clone="CH230-12818"
                                                                                               /sex="Female
                                                                                                        /clone_lib="CHORI-230 segment 1"
                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                 strain="BN/SsNHsd/MCW
                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type-"Lymphocytes"
/note-"Vector: pBACe3.6; Site_
RPCIII Human Male BAC Library"
103 c 97 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RPCI-11-110C18"
/clone_lib="RPCI-11"
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Jong
64 g
                                                                                                                                                                                                                                                                  column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.6; DB 17
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
       181 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                               MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geer,K., Shvartsbeyn, Chen,D., Riggs,F.,
                           Site_2: EcoRI; produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 30-NOV-2001
genomic clone
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SOURCE
ORGANISM
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VERSION
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AQ776894/c
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                ACCESSION
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AZ397654 560 bp DNA linear IM0162D13R Mouse 10kb plasmid UUGCIM library Mus clone UUGCIM0162D13 R, DNA sequence.
AZ397654 AZ397654.1 GI:10512726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ776894 1.1 AZ_B07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=886 Col=14 Row=C, DNA sequence: AQ776894 G1:5679854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 552.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.htsc.washington.edu
Plate: 886 row: C column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
l (bases 1 to 552)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ibrary availability, please contact Pieter de Jong
pieter@dejong.med.buffalo.edu). Clones may be purchased from
PACPAC Resources (http://bacpac.med.buffalo.edu/ozdering_bac.htm
pr from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                canning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCGTGGGATAGTCCGTCATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Igh Throughput Sequencing Center
liversity of Washington
liven Anne Avenue North, Seattle, WA 98109, USA
1: (206) 616-3618
ax: (206) 616-3887
                                                                                                                                                                                             TTCGTGGGATAGTCCGTCATGGTGT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTAGAGGGATAGTCAGTGATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ail: jwallace@u.washington.edu
ones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                   Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

1 114 c 92 g 139 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=886 Col=14 Row-C"
/clone_111-"RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                               66.48;
                                                                                                                                                                                                                                                 Score 18.6; DB 17;
Pred. No. 6.6e+02;
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                                                   genomic
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VERSION
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BH265153/c
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse
                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                       118 a
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male
                                                                                                                                                                                                                                             66.4%;
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BH265153 635 bp
CH230-55121.TJ CHORI-230 Segment 1
CH230-55121, DNA sequence.
BH265153
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High quality sequence stop: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0162 row: D column: 13
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center University of Utah
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                                                                                                                                                                                                                                                               TTCGTGGGATAGTCCGTCATGGTGT- 27
                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/clone="UUGC1M0162D13"
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/strain="C57BL/6J"
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0;
                                                                                                                                                                                                                                                                                                                                          Score 18.6; DB 17;
Pred. No. 6.6e+02;
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Sciurognathi; Muridae;
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s genomic clone
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REFERENCE
AUTHORS
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AZ291296/c
                                                                                                                                                                  KEYWORDS
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AUTHORS
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Best Local
                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                         Local
Contact: Shaying Zhac
          Unpublished (1999)
Other_GSSs: RPCI-23-131N12.TV
                                        Mouse BAC End
                                                        and Fraser, C.M.
                                                                                                            Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                               RPCI-23-131N12.TJ RPCI-23
                                                            hao,S., Nierman,W., Feldblyum,T.,
B., Levins,M., Mcgann,S., Tsegaye,
                                                                                                                                                                              12291296.1 GI:9533082
                                                                                                                                                                                                                                     AZ291296
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                     DNA sequence.
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                                                                                                                                                                                                                                                                                                              GTTCGTGGGATAGTCCGTCATGGTG
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Rat BAC End Sequent
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao, S., Shetty, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying
                                                                                               (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epartment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ones are derived from the rat BAC library CHORI-230 http://www.chori.org/Dacpac/rat230.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             231 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute for Genomic Research Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 635)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gebregeorgis, E., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _GSSs: CH230~55I21.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          szhao@tigr
                                                                                              1 to 640)
                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by Pieter de Jong"
117 c 81 g 206 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="BN/SSNHSd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
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                                 Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                               66.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type-"Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "CH230-55121"
                                                                                                 Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                axon:10116"
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                            Score 18.6; DB 17;
Pred. No. 7e+02;
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                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                            640 bp
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                                                            Tsegaye,G.,
                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                            musculus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                        Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsegaye,G., (
, Russell,D.,
                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MD 20850,
                                                    Geer, K., Krol, M., de Jong, P
                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                           linear
                                                                                                  Muridae;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                     Shatsman, S., Akinret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (pdejong@mail.cho.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geer,K., Shvartsbeyn, Chen,D., Riggs,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                        635;
                                                                                                            Euteleostomi;
                                                                                                                                                                                                        GSS 27-JUL-2000
PRPCI-23-131N12
                                                                                               Murinae; Mus
                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                            Gaps
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FEATURES
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AUTHORS
TITLE
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
BG293648
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 GTTCCAGGTATAGTCCATCATGGTG
                                                                                                                                 Contact: "Correction of the Copko Laboratory Tissue Procurement: The Cepko Laboratory Preparation: Life Technologies, a.c. E. Cons
       High quality sequence start: 358 High quality sequence stop: 717.
                                                                                                                                                                                                                       NIH-MGC http://mgc.nc1.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                              Plate: LLAM10371
                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                           cDNA Library Preparation: Life Techno cDNA Library Arrayed by: The I.M.A.G.
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG293648
                                                                                                                                                                                                                                                                                                                                                                                                                                      BG293648 736 bp m
602390516F1 NIH_MGC_94 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                EST
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                                                                                                                                                                                                                                                                                                                                                           nouse mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC clones are derived from the mouse BAC library PRCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCGTGGGATAGTCCGTCATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                 (bases 1 to 736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note organ: Kidney/Brain; Vector: pBACe3.6; Si
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidno
brain genomic DNA was isolated and partially did
with a combination of EcoRI and EcoRI Methylase.
selected DNA was cloned into the pBACe3.6 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECORI Sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RPCI-23-131N12"
clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.4%;
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                                            row: o column:
                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Rockville,
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                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                             gies, Inc.
Consortium
                                                                                                                                                                                                                               Gene Collection (MGC)
                                                                                                                                                                                                                                                                                     Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         partially digested
                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE: 4502619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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BH267142/c
BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                           availability, please contact Pleter de Jong (pdejong@mail.cho.o.) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Other_GSSs: CH230-55010.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org

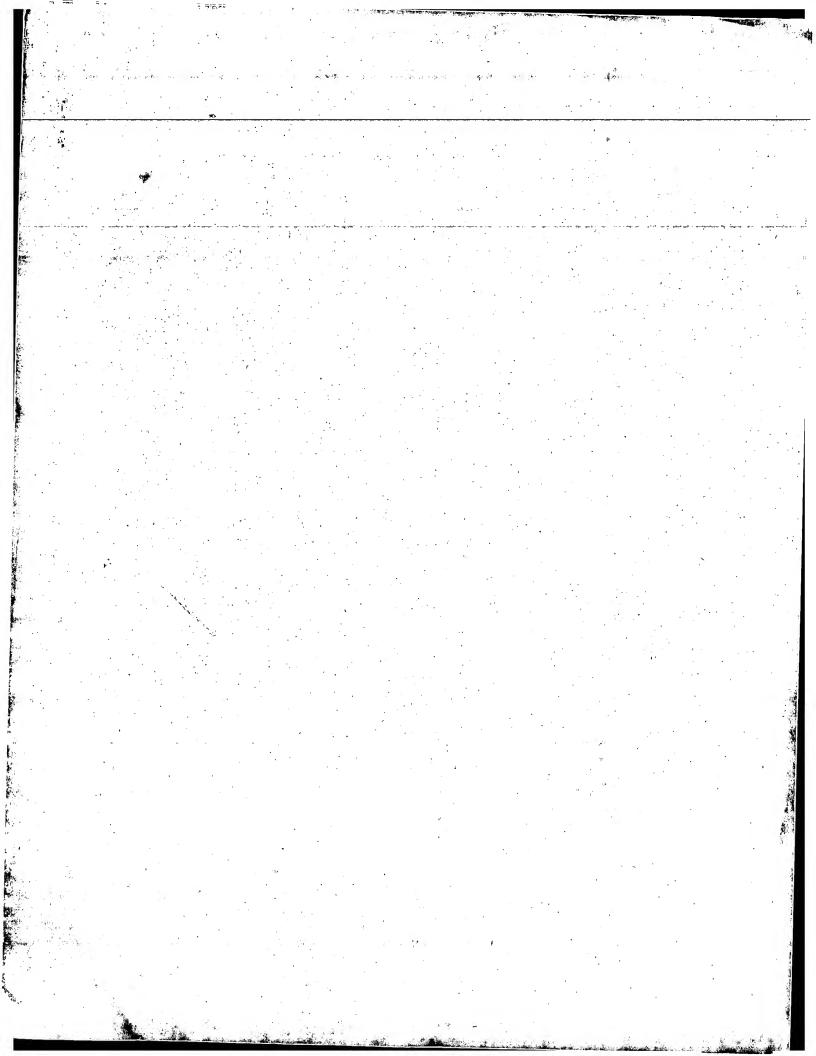
lones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC End Sequences from Library CHORI-230 EcoRI segment
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                       275
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                                         Pieter de Jong"
                                                              /note="Vector: pTARBAC2.1; Site_1: ECORI; Site_2: ECORI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
160 c 210 g 185 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed
                                                                                                                                                                                                                                                                                            Pocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="NIH_MGC_94"
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                                                                                                           cell_type="Brain"
                                                                                                                                                                                                   'strain="BN/SSNHsd/MCW"
'db_xref="taxon:10116"
                                                                                                                                                                                                                                           organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'tissue_type="retina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:17179062
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                                                                                                                                                                                                                                                                                       ion/Qualifiers
                                                                                                                                  emale"
                                                                                                                                                       _lib="CHORI-230 Segment 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.6; D
Pred. No. 7.4e
0; Mismatches
                       251
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                                                                                                                                                                                                                                                                                                                                                                                                                                              de Jong (pdejong@mail.cho.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 30-NOV-2001
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SOURCE

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BH279359/c
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113 GTTAGAGGGATAGTCAGTGATGGTG
                2 GTTCGTGGGATAGTCCGTCATGGTG 26
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail
Clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                   page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 128 row: C column: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hao,S., Shetty,J., S
A., Gebregeorgis,E.,
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BAC End Sequences from Library CHORI-230 EcoRI segment
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301 838 0208
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                                                                                                                                           Pieter de Jong"
139 c 109
                                                                                                                                                                          /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                         /db_xref="taxon:10116"
/clone="CH230-128C8"
                                                                                                                                                                                                                         /sex="Female"
                                                                                                                                                                                                                                                                                         /strain="BN/SsNHsd/MCW"
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, Russell,D.,
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Search completed: July 11, Job time : 510.434 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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## SUMMARIES

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# ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	RESULT 1 AL133229
Direct Submission	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 161776)	Homo sapiens	human.	HTG; CpG island.	AL133229.40 GI:8546579	AL133229	STSs, GSSs and a CpG island, complete sequence.	Human DNA sequence from clone RP5-1167E19 on chromosome 20 Contains	AL133229 161776 bp DNA linear PRI 06-APR-2001	

Pred. No. is the number of results predicted by chance to have a

repeat_regi	repeat_regi	repeat_regi	repeat_regi	repeat_regi	misc_featur	misc_featur	repeat_regi	repeat_regi	repeat_regi	repeat_regi	repeat_regi	repeat_regi	repeat_reg	repeat_reg	misc_featu	misc_featu			source	PEATITIES VEC	htt	ass the	as one	chem 30);	reg	tru	in.	Mai	- ₩ - ₩ - 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1 = 1	0.0	The	· · · · · ·	va. Va.	COMMENT On Du	ed ED FOR THINKSOOD	
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                                                                                                                                                                                                                                                                                        AC022646 166523 bp DNA linear HTV Homo sapiens clone RP11-28C18, WORKING DRAFT SEQUENCE,
          Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
                                                                                                Homo
                                                                                                                 Birren,B., Linton,L.,
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1 (bases 1 to 166523)
                                                                                                                                                                                   Homo sapiens.
Homo sapiens
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/note="match: STS: Em: 294
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Pred. No. 3
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                                                                                                               Nusbaum, C.
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                                                                                                                 and Lander, E.
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On Mar 16, 2000 this sequence version replaced gi:6984422. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein
Landers,T., Lehozky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGürk,A., McKernan,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tirrell, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pierre, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It current consists of 18 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runs of N, but the exact sizes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 5.2 in Q20 bases; agarose-fp Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 15734 bases at least Q30 Consensus quality: 161890 bases at least Q30 Consensus quality: 163469 bases at least Q20
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Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 156000; agarose-fp
Insert size: 164823; sum-of-contigs
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                                                                                                                                                                                                                                                                               7280: contig of 1443 bp in 7281 7380: gap of 100 bp 1381 11595: contig of 4215 bp in 11596 11695; gap of
                                                                                                                                 27816
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15: gap of 100 bp
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  gap of 1
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35: contig of 11492
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              Human DNA sequence from clone RP11-733D4 on chromosome 10,
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AL356157
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misc\_feature repeat\_region repeat\_region

'note="match: GSS: Em:AQ531274 Em:AQ546391 Em:AQ625817

e="AluSg repeat: matches 54. .310 of consensus" 5. .14589

repeat: matches 3424. .4101 of consensus

\_repeat: matches -243...3424 of consensus

repeat\_region repeat\_region repeat\_region

note="LIPB1 repeat: matches 4101. .6155 of consensus" 0553. .11064

repeat:

matches 1.

.511 of consensus"

repeat: matches 2321. .2614 of consensus

.312 of consensus"

misc\_feature

1059. .1224 /note="MIR repeat: matches 33. .195 of consensus"

'note="U2 repeat: matches 2.

.36 of consensus"

clone\_lib="RPCI-11.3" 'clone="RP11-733D4"

repeat\_region

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> note="AluSx repeat: matches 1. note="match: GSS: Em:AQ103508"

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FEATURES
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AUTHORS
TITLE
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KEYWORDS
SOURCE
ORGANISM
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                                                         source
                                                                                                                  The true right end of clone RP13-37403 is at
                                                                                                                                 This sequence is the entire insert of clone RP11-733D4 The true left end of clone RP11-523E20 is at 189958 in this sequence. The true right end of clone RP11-256K7 is at 98701 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                       chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponding to the overlapping clone, as we submit sequences with overlap as described above.

This sequence was finished as "for a submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                             latabase can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 198917)
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                                                                                                                                                                                                                                                                                                                                                                 p://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence generated from part of bacterial clone contigs of human
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                                                                                                                                                                                                                                     //www.chori.org/bacpac/home.htm
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                                                      Location/Qualifiers
1. .198917
organism="Homo sapiens"
db_xref="taxon:9606"
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                               Lem<sup>®</sup>MIR repeat: matches 54. .41249
                                                                                                          "MER5B repeat: matches 96. .148 of consensus
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                                                                                                                                       "LIMC3 repeat: matches
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                                                                                                                                                                                                                             "L1P4 repeat: matches 5492. .5781 of consensus"
                                                                                                                                                                                                                                                                                                                          "LIMD3 repeat: matches 5913. .6401 of consensus"
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                                                                                                                                                                                  AIUY repeat: matches 35.
                                                                                                                                                                                                                                                                                                                                                                                     "MLTID repeat: matches 240.
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мік repeat:
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                                                                                                                                                                    repeat: matches 3825.
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

bacteriophage phi-12.
bacteriophage phi-12
Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
1 (bases 1 to 6751)

AF408636 6751 bp ds-RNA 13 Bacteriophage phi-12 P14 (14), P15 (15), cor RNA-dependent RNA polymerase P2 (2), NTPase structural protein P1 (1) genes, complete cd

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                                                                                                                                                                                                                                                                                                                                                                                                        plement(58158.
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-e-"L2 repeat: matches 2662.  
plement(57923. .58306)
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3. .54633
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6. .49349
e="MER20 repeat: matches 1.
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7. .54341
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. .44845
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                                                                                                                                                                                                                                                         .59806
                                                                                                                                                                                                   LIM4 repeat: matches 867.
                                                                                                                                                                                                                                                                    repeat: matches 1543. .1831 of consensus
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GSS: Em:AQ140587"
310. .58614)
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Submitted (10-AUG-2001) Microbiology and Immunology, Sophie Davis School of Biomedical Education, City College of New York, 138th Street and Convent Avenue, New York, NY 10031, USA
Location/Qualifiers
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Characterization of
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EEVWRVFDDTYATLMEPHYGSFLGIVQRAHKEIPFSVDDLSWKEIMVLDDPNKMYHRF
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                                                                                                                                                                                                                                                                                                 KIAGFLECKHAFFGDVSSYDHSFSEEKIDLSLEVGKEFISPEIMELASSLFYAAYFTR
PLGPDDGPQLVGNPNRYLEKQVKAGNRSGHAFTSLFAKVWKVIDTVSKFDQMGYDVVA
                                                                                                                                                                                                                                                                                                                                                                                                      KRANAVAQPDINSDGFSINGLHTTFDSIRSVSGYPOWPVSALPKSNVGLLRDIKIQER
MTARQVVIAREIWKRYWGHMKPTAIKIPKMSTSGPPRVVNDAEMKLQYALALFSGNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mmptnespkhaetrivtdaprnsesvgdhlfnggvnhhdedpda
ytkmygplvgydprnpttlfanarqtgtqlvaprkareiltgiyspeptvlafqrefv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="RNA-dependent RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mdfitdmsknorlelonrlagyetslmymshngdvpvitgfnym
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ELGALHEVSMYRVLNDIADEQLVKANMTSAELELSETKRQEAQRARKDGTVRPLVDFD
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protein_id="AALO1106.1"
db_xref="GI:15488105"
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/product="P14"
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"db_xref="GI:15488103"
"translation="MRKGDRKHMNOKPDLTYTSDVVNRRTKNYRRVAMSKQYWEDCGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTOTEIN_id="AAL01105.1"
Ib_xref="G1:15488104"
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IGREDIPGTAKGNHAILLCMDGSVFROMMIDHAPRGTKIEIIRPDNTSHTYEYLG"
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on of Bacteriophage phil2
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gandyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Cardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J., Lieu, C., Locke, K., MacGonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Morman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Changara, M., Marchan, M., McKernan, R., Roy, A., Santos, R., Severy, P., Changara, M., Marchan, M., Marchan, M., Santos, R., Severy, P., Changara, M., Marchan, M., McKernan, R., Roy, A., Santos, R., Severy, P., Changara, M., McKernan, M., McKernan, R., Roy, A., Santos, R., Severy, P., Changara, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan, M., McKernan
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AC013516 GI:9112504
HTG; HTGS PHASEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TGGAATCGGTCCTTCGTCGTCTCACCTCC TGGACTCAGTCCTTGGTCATCTCACCTTC 29

4477

13-JUL-2000

Conservative

0; Mismatches

5

0;

Gaps

Length 6751; Indels

(bases 1 to 30265)

en, B., Linton, L., Nusbaum, C. and Lander, E sapiens, clone RP11-115K5

sapiens

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70.0%;
Similarity 82.8%;
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                                                                                                                                               AQLLSDKALFTRVLDLEEDKRTVEKERYSFNVKVGAETISGAVVTTEVGMQELPDEAR
FVVPVHKLVMDTIAAIHSSFNELINAAKKVASEPFGGEDGTDLDVSNIAVTPQLVSF
MNLSRSRAILTFAQSVPPQYRQLVASVMRMRAVANKSASDILRURGTMQQQSFNAYAD
                                                                                                                                                                                                                           GPEKDVEWIYSTHTEYNRFVDLQWATCYLPGGEFITSDVGLFLLVTKDIAPTAEVEPR
                                                                                                                                VLGLVLILATNGLSSKFIRDLLEDASMVEAIMLTGSDRVKN"
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NAITHLAETGDPRSFYNGEGGSAYAKVIGEAFFLGDDGENFSKELVALMADACYLNYT
                                                                                                                                                                                                                                                                                                             TVSIADLSLDLAAQNAVRVAETVNVRMHESGKNSKLAVARAFGEALVAIGYELHRSVN
VQHIFDDIVKAIHVKLLAAASADMVGEVDSRWLHHPIVDEMSRNYTFVSAALDNPIGG
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/protein_id="AAL011
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PVLAIGVESGDAIVFDKNAQRIVAYKEKSVKAEDGSVSVVQVENGFMKQGHRGWLVDL
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/protein_id="AALO1108.1"
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            will be sequenced to completion. In the event that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeats were identified using RepeatMasker: t, A.F.A. & Green, P. (1996-1997)
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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1890
Center clone name: 115_K_5
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77 11826: gap of 91 1726: contig of 836 bg
77 11826: gap of
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2 9131: ~
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7229: cor
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10790: contig of 795
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12605: contig of 779
05: gap of 100 k
13525: contig of 820
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1682: contig
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12: gap of 100 bp
18731: contig of 789 bp
31: gap of 100 bp
19608: contig of 777 bp
                                                                                                             100 bp 16131: contig of 843 bp
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                                                   p of 100 bp
contig of 809 bp
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contig of 776 k
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                                                                                                                                      contig of 714 bp in
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                                                                                                                                                                                                                                                                                                                                    Human DNA sequence from clone RPI-32I10 on chromosome 22 Contains a pseudogene similar to TCEBIL (transcription elongation factor B (SIII), polypeptide 1-like), a CA repeat (D22S1159), STSs and GSSs., complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                                                                                     On Aug 24, 1997 this sequence version replaced gi:1841910. During sequence assembly data is compared from overlapping clones Where differences are found these are annotated as variations
                                                                                                                                                Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                             corresponding to the overlapping clone, as we only a small overlap as described above.
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 93312)
                                                                          variation annotation may not be found in the sequence submission
                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                             285994.1 GI:2342582
                                                                                         together with a note of the overlapping clone name. Note that the
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e key.  Ilowing abbreviations are used to associate primary accessing yaven in the feature table with their source databases:  MBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP, Information  WWW.sanger.ac.uk/Projects/C_elegans/wormpep This sequence  some 22, constructed by the Sanger Centre Chromosome 22  yaww.sanger.ac.uk/HGP/Chr22  yaww.sanger.ac.uk/HGP/Chr22  Ilo is from the library RPCI-1 constructed at the Roswell  ancer Institute by the group of Pleter de Jong. For further  s see http://bacpac.med.buffalo.edu/	feature key The following abbi numbers given in 1 Em: EMBL; Sw: Sy on the WORMPEP dat http://www.sanger. was generated from chromosome 22, con Mapping Group. Fut http://www.sanger. RPI-32IIO is from Park Cancer Instit Park Cancer Instit OECTOR: DCYPAC2	

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                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                  University, 4444 Forest 5 (bases 1 to 141313)
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COMMENT
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                                                                                  Submitted (22-MAY-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                               Direct Submission
Center project name: H_DJ0991G20
               Contact: sapiens@watson.wustl.edu
                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                  Web site:
                                          http://genome.wustl.edu/gsc
                                                                                                              gi:3924671.
                                                                                                                                 USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence restriction digest. irom more than one subclone; and the assembly was confirmed ьy

### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis McPherson and information about the map position of this sequence, see http://genome.wustl.edu/gsc

#### SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-5, prepared Pieter de Jong and coworkers at http://www.chori.org using the method described by Joannou et al., Nature Genetics 6:84-9 (1977) The library is from one male donor. The clone may be obtained either from Genome Systems, http://www.genomesystems.com) or Research http://www.resgen.com); or from Pieter de Genetics, Inc. (1994).

# NEIGHBORING SEQUENCE INFORMATION:

PCYPAC2

The clone sequenced to the right is CTD-2532L16, 200 bp overlap. Actual start of this clone is at base position 1 of RP5-991G20; actual end is at base position 141313 of RP5-991G20.

repeat_region	repeat_region	repeat_region	. repeat_region	repeat_region	repeat_region	repeat_region		mico feature	repeat_region	repeat_region				•		source	FEATURES
42854342	/*pcram_ry	396. 3517	/rpt_family="A1" /rpt_family="A1"	2743	23522613 /rpt family="Alu"	.21232228 /rpt family="L2"	/note="similar to EST W87623 (NID:g1401687) zh65h0	/rpt_family="L2"	12191292	85235 /rpt_family="MIR"	/clone_lib="RPCI-5"	/clone="RP5-991G20"	/map="16"	/chromosome="16"	/db_xref="taxon:9606"	1141313	Location/Qualifiers

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GSNTFTTSNPSSAGIAPSSNILLSQVPTESVGMPPLGNPIGANIASPSEFKEANRKKLA
                                                                            /translation="EAIEDVEGPSETAADPEELAKDQEGGASSQAEKELTDSPATSK
RISFPGSSESPLSSKRPKTAEEIKPEQMYQCPYCKYSNADVNRLRVHAMTQHSVQPML
RCPLCQDMLNNKIHAQHLTHLHSVAPDCVEKLIMTVTTPEMYMPSSMFLPAAVPDRD
GNSNLEEAGKQPETSEDLGKNILPSASTEQSGDLKPSPADPGSVREDSGFICWKKGCN
QVFKTSAALQTHENEVHAKRPQLPVSDRHVYKYRCNQCSLAFKTIEKLQLHSQYHVIR
                               AATMCCLCQRSFRTFQALKKHLETSHLELSEADIQQLYGGLLANGDLLAMGDPTLAED
HTITVEEDKEEESDLEDKGSPTGSDSGSVQEDSGSEPKRALPFRKGPNETMEKFLDPS
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                                                                                                                                                                  /product="unknown"
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/db_xref="GI:3924672"
                                                                                                                                                                                                                      note="alpha-fetoprotein enhancer-binding protein; 99% dentical to A41948 (PID:g283975); H_DJ0991G20.1"
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AVGPAQAHRRCPFCRALFKAKTALEAHIRSRHWHEAKRAGYNLTLSAMLLDCDGGLQM
KGDIFDGTSFSHLPPSSSDGQGVPLSPVSKTMELSPRTLLSPSSIKVEGIEDFESPSM
SSVNLNFDQTKLDNDDCSSVNTAITDTTTGDEGNADNDSATGIATETKSSSAPNEGLT
                                                                                                                                                          PYQCDQCKLAFPSFEHWQEHQQLHFLSAQNQFTHPQFLDRSLDMPFMLFDPSNPLLAS
QLLSGATPQTFASSATSPSTPTSTMNTLKRKLEEKASASPGENDSGTGGEEPQROKRL
RTTTTPEQLEILYQKYLLDSNPTRKMLDHTAHEVGLKKRVVQVWFQNTRARERKGQFR
                                                                                                                                                                                                                                                                                               EDDEGGODISQNEDSMDAMEILTPTSSSCSTPWPSQAYSAPAPSANNTASSAFLOLTAE
ABELATFNSKTEAGDEKFKLAERPSAQPNOTOEKGGOPKPELGOCEOPBOKTNTPOOK
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QNYFFFKQLEREAKQYRDHYDKLYPLRPQTPEPPPPPPPPPPPPPPAAPPQPASTPAI
PASAPPITSPTIAPAQPSVPLTQLSNFMELPIFSFLMMQTNPLQTLPAQLPPQLGPVE
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                                                                           Direct Submission
Submitted (20-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Mar 20, 2002 this sequence version replaced gi:19387786.
                                                                                                                                                                                   Direct Submission
Submitted (13-MAR-2002) Genome
University School of Medicine,
                                                                                                                                                    Waterston, R.
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Submitted (24-JAN-2002) Genome
University School of Medicine,
                                                                                                                                                                                                                                       Waterston, R.H.
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Isak,A., Haakenson,W. and Cre
The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 147091)
Sulston, J. E. and Materston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                           Waterston, R.H.
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24; Conservative
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                                                                                                                                                                   (bases 1 to 147091)
                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
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sapiens BAC clone RP11-100C9
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Pred. No. 37;
0; Mismatches
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Center project name: H\_NH0100C09

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Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MC. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome and coworkers at http://www.chori.org Research Genetics, ibraries. pBACe3.6 Genomics 51:1-8. Inc. (http://www.resgen.com) or Pieter de Jong The clone may be obtained either from

# NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-384K6; the clone sequenced to the right is RP11-358D17, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-100C9; actual end is at base position 34330 of RP11-358D17. this

The sequence of AC009865 has been incorporated Location/Qualifiers into AC108030

FEATURES misc\_feature .misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature repeat\_region repeat\_region repeat\_region source repeat\_region /organism="Homo sapiens"
/db\_xref="taxon:9606"
/chromosome="4" clone="RP11-100C9" clone\_lib="RPCI-11" note="match to EST BG687120 (NID:g13918517)" te="similar to Mus musculus EST BF302831 (D:911249388)" .14709 te="match to EST AU130547 te="match to EST AW805082 (NID:g7856965)," te="match to EST BI048881 (NID:g14455503)" e="similar to EST BM461794 (NID:g18510834)" e="match.to EST BG687120 (NID:g13918517)" e="match to EST AU130547 \_family="Alu" \_family="AT\_rich" family="Alu" .2814 imilar to EST BM461794 (NID:g18510834)" (NID:g10990901)" (NID:g10990901)"

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between neighboring data submissions.
                                                   NOTICE:
                                                                                                                                                     Direct Submission
Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 3, 2001 this sequence version replaced gi:14151042
                                                                                                                                                                                                                                                                                        Submitted (03-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
    OPICE: This sequence may not represent the entire insert of this lone. It may be shorter because we only sequence overlapping lone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                               Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 151552)
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                                                                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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82.8%;
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Primates; Catarrhini; Hominidae;
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome http://bacpac.med.buffalo.edu) The RPCI-11 Genomics 51:1-8. human BAC library was made from the blood of one male The clone may be obtained either from

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is AC006568.
clone is at base position 1 of RP11-415C15. Actual start of this

FEATURES The region between 36765 to 36883 is covered only by a single ocation/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                    2 (bases 1 to 15)
Worley,K.C.
Direct Submission
                                                                                                      Wu,C., Wu,Y., Wu,Y.F., Zhou, Weinstock,G. and Gibbs,R. Direct Submission
                                                                                                                                                                                        Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Watlington, S.,
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Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
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Falls,T., Ferraguto_D., Flagg,N., Ford,J., Foster,P., Fran
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Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kova
tratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
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fernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
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1,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
11,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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(16-MAY-2002) Human Genome Sequencing Center, Department
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Christopoulos, C

David, R.,

Chavez, D.,

Bryant, N.P.,

Durbin, K.J.

Korvah, J., Kovar, C.,

Hernandez, J

Frantz, P.,

Martinez; E.,

Tang,H.,

Ma',

.C., Lewis,L., Loulseged,H.,

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COMMENT
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AUTHORS
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Baylor Plaza, Houston,
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NOTE: This is a 'working draft' sequence. It currently
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Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,
Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
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Homo sapiens chromosome 3 clone RP11-316A10 map
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Li,C., Li,F., Li,G., Li,T., Liu,Y.,
N., Liu,B., Liu,Y., Li,W., Li,Y., Luo,J., Niu,Y., Qi,O.,
Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R.,
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H. Zhang, H.,
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                                                                                                                                              89672 GGGCTCAGTCCTTGGCCCTCTCCCATTCT 89700
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Homo sapiens 161,604 genomic DNA of 11q
Published only in DataBase (2000)
2 (bases 1 to 161604)
Hattori, M., Ishil, K., Toyoda, A. Taylor, T.
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1 Similarity 82.8%;
24; Conservative
Homo sapiens chromosome i
17 unordered pieces.
AC025163
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30042 30260 D1153059 Homo sapiens
32665 32849 DXS7944 X Homo sapiens
78501 78757 D1153473 Homo sapiens
127357 127571 D1154143 11 Homo sapiens
148518 148806 SHGC-172582 Homo sapiens
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Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Chemical Research (RIKEN), Genomic Sciences Center (GSC); [-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa: TE-mall:hattor1eysc.riken.go.jp, (RE:http://hgp.gsc.riken.go.jp/, rel:81-45-503-9170)
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/chromosome="11"
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/db_xref="taxon:9606"
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35161 c 35897 g 47643 t
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Primates;
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DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Watlington,S., Williams,G., Williamson,A., Wleczy
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Sequencing vector: M.3; L08821

Chemistry: Dye-primer Bodipy: 1% of reads
Chemistry: Dye-terminator Big Dye: 99% of reads
Chemistry: Dye-terminator Big Dye: 99% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 16802 bases at least Q40
Consensus quality: 180431 bases at least Q30
Consensus quality: 185136 bases at least Q20
Estimated insert size: 177736; sum-of-contigs estimation
Destinated insert size: 17736; sum-of-contigs estimation
Consensus quality: 185136 bases; agarose-fp estimation
Estimated insert size: 177736; sum-of-contigs estimation
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Bowie, S., Brieva, M.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: RP11-533F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: HAMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25, 2001 this sequence version replaced g1:12831249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Burkett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chowdhry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavazos, S.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dederich, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K., Blankenburg, K., Bonnin, D., Bouck, J., Brown, E., Brown, M., Bryant, N.P., Buha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,C., Adio-Oduola,B., Ali-osman,F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown, E., Brown, M., C., Carron, T.F.,
Burrell, K.L., Byrd, N.C., Carron, T.F.,
R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Cleveland, C.D., Cox, C.,
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I., Douthwaite, K.J., Draper, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S., Huber, J., Hulyk,
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         sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S., Hume, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tamerisa,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hale, S.
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RESULT 14
AC130278
LOCUS
DEFINITION
                                            VERSION
KEYWORDS
                                                                       ACCESSION
                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                 FEATURES
                      ORGANISM
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                            68919 GGACTCAGTCCTGGGTCCCCTTCCCTTCT 6889
                                                                                       Mus musculus clone RP24-393I16,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                     Mus musculus
                                                                                                                                                                             2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
                                          HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                            unordered pieces.
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                                 ouse mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           runs of N, but the
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                                                                                                                                                                                                                                                                      a 43543 c 42200 g
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                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a 'working draft' sequence. It currently contigs. The true order of the pieces
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he exact sizes of the gaps are unknown
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Pred. No.
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0; Mismatches
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37;
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WORKING DRAFT SEQUENCE, 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-AUG-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Connor.T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K.,Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus, clone RP24-393I16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange Thomann, N., Stojanovic, N., Talamas, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viel,R., Vo,A., Wilson,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resfaye,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barna, N., Bastien, V., Bloom, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aratas, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
forton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat
                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    u,G., MacLean,C.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 5.6 in Q20 bases; agarose-fp Quality coverage: 5.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.960731
Consensus quality: 168477 bases at least Q40
Consensus quality: 173980 bases at least Q30
Consensus quality: 176349 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid; n/a; 1
Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L2 Center clone name: 393_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 178000; agarose-fp
Insert size: 179195; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
                                                                                        0059 10158:
                                                                                                                                           7874 8549: contig of 676
8550 8649: gap of 100 b
8650 9264: contig of 615
                                                                                         8650 9264: contig of 615 L
9264: contig of 615 L
9265 9364: gap of 100 bp
9365 10058: contig of 694 b
9059 10158: ran of
                                                                                                                                                                                             1 7168: contig of 7168 bp in length
7169 7268: gap of 100 bp
7773: contig of 555 bp in length
7774 7873: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferreira, P., FitzGerald, M.,
                                               100 bp
10902: contig of 744 bp
11002: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kells,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meldrim, J., Meneus, L.,
                           gap of 11256:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Project Information
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                                 contig of 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu, X., Wyman, D., Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boguslavkiy, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L., Mihova, T., Mlenga, Nicol, R., Norbu, C., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ali, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levine, R.,
                                                                                                      bp in length
                                                                                                                                           bp in length
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                                  bp in length
                                                                   bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100% of reads
in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norman, C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamat, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rogov, P.,
                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                  source
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                                                                                                                     ector_side:left"
                                                                                                                                                                                              clone_lib="RPCI-24 Male
                                                                                                                                                                                                                                 organism="Mus musculus"
db_xref="taxon:10090"
                                                                                    note="assembly_fragment"
                                                                                                                                                          note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21353:
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                                                                                                                                           Lone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03351; con
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13682: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93: gap of 100 pp
37124: contig of 3231 bp in length
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19: gap of 100 bp
19489: contig of 2070 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22801:
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3122: contig of
                  "assembly_fragment"
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8293: contig of 5202 bp in length
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                                                                       .8549
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                                                     ssembly_fragment"
                                                                                                                                                                                                                                                                                       /Qualifiers
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contig of 23715 bp in length
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f 2204 bp in length
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AC024545/c
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                                              TITLE
       AUTHORS
                                                              AUTHORS
                                                                                                                   ORGANISM
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Best Local
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  2 (bases 1 to 193700)
Birren, B., Linton, L.,
                                                                                                                                                                                              AC024545
Homo sapiens clone RP11-442P6, WORKING
                              npublished
                                                                                                                                                                                                                C024545
                                                                                ukaryota; Metazoa; Chordata; Craniata; Veammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                       C024545.4 GI:10280888
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                         (bases 1 to 193700)
                                                                                                                                                                                                                                                                               TGGTCTCCTGCCTTGGTCATCTCACCTCC 52016
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                                         en, B., Linton, L., Nusbaum, C., sapiens, clone RP11-442P6
                                                                                                                                         HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                        Conservative
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82.8%; Pred. No.
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2. .17319
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  Nusbaum, C.,
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                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                37;
                                                      and Lander, E.
Lander, E., Abraham, H., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                             DRAFT SEQUENCE,
                                                                                            Vertebrata; Euteleostomi;
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CE, 39 unordered
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Riley, R., Spencer, B., Stange-Liberty, P., Spencer, B., Stange-Liberty, P., Spencer, B., Stange-Liberty, P., Spencer, B., Stange-Liberty, Theodore, J., Titter-Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B. Stanger, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B. Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B. Travers, M., Trigilio, J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                 Norman, C.H., O'Connor, T
Peterson, K., Pierre, N.,
                                                                                                                                                                                                                                                                         Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McDwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,
Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grand-Pierre, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galagan, J., Gardyna, S., Ginde, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DeArellano, K.,
                                                                                                oukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., hoepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., eArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Landers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grant, G., Hagos, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson, R., Jones, C., Kann, L., Karatas, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goyette, M., Graham, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beda, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heaford, A., Horton, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boguslavkiy, L.
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Submitted

COMMENT

Research; 320 Charles bmitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome search, 320 Charles Street, Cambridge, MA 02141, USA Sep 23, 2000 this sequence version replaced gi:8389572. repeats were identified using RepeatMasker:
(A.F.A. & Green, P. (1996-1997)
(http://ftp.genome.washington.edu/RM/RepeatMasker.html

Contact: sequence\_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu

Center: Whitehead Institute/ MIT Center Center code: WIBR

for Genome

Research

Center clone name: 442\_P Center project name:

Quality coverage: 3.3 in Q20 bases; agarose-fp Quality coverage: 3.3 in Q20 bases; sum-of-contigs Assembly program: Phrap; version 0.960731 Consensus quality: 167580 bases at least Q40 Consensus quality: 180250 bases at least Q30 Consensus quality: 185744 bases at least Q20 Insert size: 188000; agarose-fp Insert size: 189900; sum-of-contigs Sequencing vector: M13; M77815; 10 Chemistry: Dye-terminator Big Dye; e; 100% of 0.960731 100% of f reads b of reads

is not known and their order to are representations of N, but the exact sizes of the gaps are unknown. runs of N, but the exact sizes of the finished sequence whis record will be updated with the finished sequence whis record will be added and the accession number will NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is not known and their order in this sequence record is here. 11432 11531: gap of 100 bp 11532 13523: contig of 1992 bp in 13524 13633: gap of 100 bp 13624 16363: contig of 2740 bp in 16364 16463: gap of 100 bp 8912 9011: 2983 3082: 1683 1782: 4 5743: gap 4543: contig of 1461 bp 4643: gap of 100 bp 7389: 8911: contig of 1522 bp in 11: gap of 100 bp 11431: contig of 2420 bp in 100 bp 100 sylving of 1546 bp 19: gap of 100 bn 8911: conti-2982: con 5643: 1682: contig of 1682 bp 100 bp 1: contig of 1200 bp p of 100 1 contig of 1000 bp bp in length đđ in in length in length Ħ 'n length length length length length length

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3 36641: contig of 2
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'note-"assembly_fragment"
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33682: contig of
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                    e="assembly_fragment"
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353: gap of 10
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349: gap of 10
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9346: contig of
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736: contig
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407: contig of
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GGACTCAGTCCTTGGTCATCTCACCTTCT 30 	70.0%; Score 21; DB larity 82.8%; Pred. No. 37; Conservative 0; Mismatches	/note="assembly_fragment" /note="assembly_fragment"	a :		.48341										.16363					46445643 /note="assembly_fragment"
56 	2; Length 193700; 5; Indels 0;		.*		•	•			:						٠					

Search completed: July 10, 2003, 19:20:11 Job time: 269.955 secs

0;

Gaps



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Minimum DB seq
Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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1067.241 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/qcqdata,
                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:
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                                       AAT39735
AAV15324
AAL40116
AAX60950
AAX60951
AAT11268
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         Pathogenic microor
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
                                                                                                                                  Description
                                                                                         Hepatitis C virus Hepatitis C virus
    RESULT 1
Replication of hepatitis C virus in non-lymphoblastoid mammalian
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22
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#### ALIGNMENTS

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AAT39735/c
ID AAT39735 standard; DNA; 36 BP.
                                                                                                                                                                                                   15-AUG-1996.
                                                                                                                                                                                                                                    WO9624662-A1
                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus; HCV; polymerase chain reaction; amplification; replication; non-lymphoblastoid cell; monkey kidney cell;
                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1997
WPI; 1996-384435/38.
                                  Battaglia M,
Ravagnan G;
                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                               hybridisation probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT39735;
                                                                                        (CNDR ) CONSIGLIO NAZ DELLE RICERCHE.
                                                                                                                             10-FEB-1995;
                                                                                                                                                                10-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus PCR probe S1, based on nucleotides 121-157.
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                    Carloni G,
                                                                                                                             95WO-IT00016
                                                                                                                                                                95WO-IT00016.
                                                      Iacovacci S,
                                                        Ponzetto
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useful for studies

of HCV

replication,

prodn.

of.

0,

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RESULT 2
AAV15324/c
ID AAV15324
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Best Local
     mixture having a Mg2+/Tag polymerase racto or country DELA (DNA enzyme unit; and (c) detecting the amplification product by DELA (DNA enzyme immunoassay) using an oligonucleotide probe. The sensitivity of this immunoassay
                                                        The present sequence represents a probe involved in the method of the present invention for detecting hepatitis C virus (HCV). The method comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the resulting CDNA by a single polymerase chain reaction in a reaction
using nested
                                                                                                                               Disclosure; Page 4; 26pp; English.
                                                                                                                                                        Detection of hepatitis C virus - single-step PCR and detection by
                                                                                                                                                                                                 WPI; 1998,-042222/04.
                                                                                                                                                                                                                              Bosio P,
                                                                                                                                                                                                                                                      (WESA )
                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             washed and incubated under growth conditions. In an example, the presence of HCV in culture medium of monkey kidney cells inoculated with HCV infected serum was verified by PCR amplification using two external primers (OUI and OUZ, see AAT39731 and AAT39732) and two internal primers (INI and INZ, see AAT39733 and AAT39734). The amplified products were identified by hybridisation to labelled probe S1 (see AAT39735). Small amounts of virus were shown to be released into the culture medium from secondary cultures. Control (non-inoculated) cells were negative for presence of viral genome.
                                                                                                                                                                                                                                                                                                             03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                    11-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                WO9746716-A1
                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV15324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 BP; 9 A; 9 C; 11
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viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infecting amount of HCV has been absorbed. Infected cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus can be replicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - useful
antigens,
                                          ng cDNA by a single polymerase chain reaction in a reaction having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                               immunoassay;
                                                                                                                                                                                                                                                       WABCO BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                           Clemenza F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGTGTACTCACGGTTCCGCAGACCACTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTGTACTCACCGTTCCGCAGACCACTATGG 32
                                                                                                                                                                                                                                                                                                                                                                                         C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C virus probe HCV40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         first incubating an HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                              C virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 8; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                 96IT-M000404
                                                                                                                                                                                                                                                                                                         97WO-IT00128
                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; detection; reverse transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                               RNA;
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                                                                                                                                                                  reverse transcription,
                                                                                                                                                       enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in non-lymphoblastoid mammalian
                                                                                                                                                    immunoassay
    more complicated assays
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                                                                                    The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                       probe;
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RESULT 4
AAX60950/c

B Qy

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CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33

CGGTGTACTCACCGGTTCCGCAGACCACTATGGC

38

Query Match
Best Local Similarity
Matches 33; Conserv

Conservative

66.7%; 97.1%; 14

Score 22; Pred. No.

В

24;

Length 41; Indels

1:

Gaps

Mismatches

Sequence 41

BP; 7

A;

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11 T; 0 other;

ΧIJ

AAX60950 standard; DNA; 68

ВP

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RESULT 3
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                            The invention relates to a probe containing a 410 or 20 base pair sequence, given in the specification. It is capable of detecting the tuberculosis bacterial group including Mycobacterium tuberculosis, Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti and/or Mycobacterium canotti. The method is useful in disease diagnosis and monitoring therapy. This polynucleotide sequence represents a PCR primer relating to the detection of pathogenic microorganisms of the
                                                                                                                                                                                                                                                                                                  26-DEC-2000;
26-DEC-2000;
29-JUN-2001;
13-SEP-2001;
                                                                                                                                                 Claim 57;
                                                                                                                                                                   Detecting pathogenic microorganisms with oligonucleotide probes primers, useful in disease diagnosis and monitoring therapy
                                                                                                                                                                                                                   WPI; 2002-500769/53.
                           invention
                                                                                                                                                                                                                                               Shimada
                                                                                                                                                                                                                                                                        (TAKI )
                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                               04 -JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200252043-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monitoring therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathogenic microorganism detecting PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL40116 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL40116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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                                                                                                                                                                                                                                                                      TAKARA SHUZO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TGTACTCACCGTTCCGCAGACCACTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                            Page 97; 106pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTACTCACGGTTCCGCAGACCACTATGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                              Hino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B₽;
                                                                                                                                                                                                                                                                                                  2001JP-0278920
                                                                                                                                                                                                                                                                                                                             2000JP-0396222
2000JP-0396321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                  2001WO-JP11422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium; bovis; BCG; africanum; microti; canotti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; 7 C; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogenic
                                                                                                                                                                                                                                            Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.0%;
96.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27.4; DB 1 Pred. No. 0.0072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        microorganism; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
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AAX60950;

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                                                                                                                                                                                                                                                                                                 hepatitis G (HGV), or HIV, fungl, protozoa, parasites or mycoplasma. The method can be used to detect the presence of genetic mutations which have diagnostic or prognostic value. Pathogen contamination of food and drink supplies can also be detected using the method. The method provides for the sensitive and specific detection of ss PN analytes at concentration as low as 0.1fg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                 Sequence 68
                                                                                                                                                                                                                                                                                                                                                 probes which hybridize to the analyte and are bound to a solid support probes which hybridize to the analyte and are bound to a solid support where double-stranded (ds) polynucleotides are detected. The method can be used for detecting ss PN analytes for the detection of pathogens such as bacteria, viruses such as hepatitis C (HCV), hepatitis B (HBV), as because of mycoplasma. The hepatitis G (HGV), or HIV, fungi, protozoa, parasites or mycoplasma. The
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a new method for detection (ss) polynucleotide analytes that comprises using ss
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 65; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of single-stranded polynucleotide analytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mantero G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09928503-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-1999
                  Synthetic.
Hepatitis C virus
                                               Nucleic acid detection; pathogen; bacteria; virus; hepatitis C virus; HCV; hepatitis B; HBV; hepatitis G; HGV; HIV; fungus; protozoa; ss; parasite; mycoplasma; genetic mutation; food contamination; probe.
                                                                                                                                                   AAX60951 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999
                                                                                        Hepatitis C virus (HCV) biotinylated probe alpha-3CH.
                                                                                                             16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIAS-) DIASORIN INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid detection; pathogen; bacteria; vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-371139/31.
                                                                                                                                                                                                     40
                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mycoplasma;
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                  BP; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97IT-RM00749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US24494.
                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                 A; 17 C;
                                                                                                                                                                                                                                                  66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic
                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biotinylated
                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                  24 G; 13 T; 0 other;
                                                                                                                                                                                                                                                    Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation;
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteria; virus; hepatitis C virus;
G; HGV; HIV; fungus; protozoa; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe
                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                food contamination; probe.
                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                            Length 68;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                       ss polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                 of single-stranded
                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                          Gaps
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Claim 2; Page 9; 12pp; Japanese
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RESULT 6
AAT11268
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ss) polynucleotide analytes that comprises using ss polynucleotide probes which hybridize to the analyte and are bound to a solid support where double-stranded (ds) polynucleotides are detected. The method can be used for detecting ss PN analytes for the detection of pathogens such as bacteria, viruses such as hepatitis C (RfV), hepatitis B (HBV), hepatitis G (HGV), or HIV, fungl, protozoa, parasites or mycoplasma. The method can be used to detect the presence of genetic mutations which have diagnostic or prognostic value. Pathogen contamination of food and drink supplies can also be detected using the method. The method provides for the sensitive and specific detection of ss PN analytes at concentration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 66; 73pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mantero G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1997;
  Hepatitis C virus (HCV) anti:sense gene expression in vivo for treatme
                                                                                                                                             13-MAY-1994;
                                                                                                                                                                                   13-MAY-1994;
                                                                                                                                                                                                                           21-NOV-1995
                                                                                                                                                                                                                                                                   JP07303485-A.
                                                                                                                                                                                                                                                                                                       Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                               hepatitis C virus; clone 2-1; ss.
                                                                                                                                                                                                                                                                                                                                                                  Antisense; therapy; complementary; HCV; 5'-untranslated region; hepatitis C virus; inhibition; infection; treatment; stem-loop;
                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus partial 5'-UTR antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT11268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 68 BP; 13 A; 24 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new method for detection of single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of single-stranded polynucleotide analytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DIAS-) DIASORIN INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-NOV-1998;
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                                                               WPI; 1996-035187/04
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                                                                                                     (TOFU ) TONEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             low as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
Similarity 97.1%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · Primi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                             94JP-0124609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 G;
i:sense RNA - inhibits HCV structural treatment of HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                               RNA AS3
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RESULT 7
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Best Local
Matches 2
                      involves use of the ligase dependent polymerase chain reaction method (LD-PCR). In this method, two probes are provided. The first probe contains a region at the 5' end which is complementary and will hybridise with the TNA, the 3' end of the first probe is generic and is bound to one half of a ligand binding pair (LBP). The second probe contains a region at the 5' end which is complementary region of the first probe. It is immediately adjacent to the complementary region of the first probe. It is a conventional ligase. The TNA, they can be ligated together using binding the first probe to a paramagnetic bead to which is attached the probe complex which can then be detected either by a label attached to the second probe, by using an external probe or by PCR using the ligated.
                                                                                                                                                                                                                                                                                                Ligation dep
                                                                                                                                                                                                                               A novel
                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                      neoplasi
                                                                                                                                                                                                                                                                                                                                           WPI; 1996-058427/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a specificary is complementary (i.e. antisense) to part of the 5'-untransition region of the hepatitis C virus genome sequence contained in clone 2-1. The 5'-UTR includes several stem-loop sequences. The antisense RNA is useful for inhibiting expression of HCV structural genes and thereby inhibiting viral replication in vivo. The antisense therapy inhibiting viral conventional interferon treatment of HCV
                                                                                                                                                                                                                                                                                                                                                                      Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                               TNUOM ( NUOM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 - JUN - 1|995 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-1996 (first entry)
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          capture probes AAT09176-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dependent polymerase chain reaction; LD-PCR; probe; hybridisation; binding pair; ligase; paramagnetic bead; primer; amplification; tis; untranslated region; UTR; rRNA; ss.
                                                                                                                                                                                                                                                    5; Page 54; 100pp;
                                                                                                                                                                                                                                                                                         dependent polymerase chain reaction - ns pathogens and abnormal human genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGUGUACUCACCGGUUCCGCAGACCACUAUGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 BP;
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                                                                                                                                                                                                                                                                                                                                                                                               SINAI SCHOOL
                                                                                                                                                                                                                of detecting a target nucleic acid (TNA) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0263937
                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US07671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
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                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                               MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligated amplified sequence.
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are used to isolated a region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 G; 14 U; 0 other;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                         the detection HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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CGGTGTACTCACC-GTTCCGCAGACCACTATGGC

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Gaps

Query Match Best Local

Similarity

66.7%; 97.1%;

Score 22; DB Pred. No. 2.4; 0; Mismatches

DB 18; 6 other;

Length 120

Conservative

0;

Sequence 120 BP; 21 A; 37 C;

34 G;

22 T;

Matches

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PA
YX
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AAT69054/c
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Best Local
                Hepatitis B virus (HBV) and hepatitis C virus (HCV) can be analysed simultaneously using specific sets of PCR primers. Specifically, viral nucleic acids are isolated by treating human serum with a guanidine isothiocyanate containing solution. HBV and HCV nucleic acids are then absorbed on silica and a first polymerase chain reaction is performed using primers HB-1 and HB-2 (AAT65089 and AAT65090) and HC-1 and HC-2 (AAT65093 and AAT65094). A second PCR is then performed with the primers HB-3 and HB-4 (AAT65091 and AAT65092) and HC-3 and HC-4 (AAT65095 and AAT65095). A PCR fragment of 258 bp is produced for HBV and a PCR fragment of 163 bp is produced for HBV and a PCR fragment of 163 bp is produced for HBV and represents a fragment from HCV.
                                                                                                                                                                                                Example 3; Page 7;
                                                                                                                                                                                                                               chain reaction
                                                                                                                                                                                                                                           Simultaneously
                                                                                                                                                                                                                                                                     WPI; 1997-191071/17.
                                                                                                                                                                                                                                                                                                                             (MUNI/) MUN
                                                                                                                                                                                                                                                                                                                                                          22-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                КК9508291-в1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT69054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT69054 standard; DNA; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus 5' untranslated region the ligated amplified region created by amplification probes amp-probe-2 and -2A sequence can subsequently be detected by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 120 BP; 26 A; 34 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the primers AAT09181-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTGTACTCACCGGTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                      analysing hepatitis B and C
                                                                                                                                                                                                                                                                                                                                                         92KR-0006826
                                                                                                                                                                                                                                                                                                                                                                                    92KR-0006826
                                                                                                                                                                                             12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on; amplification; hepatitis B virus; HBV; simultaneous analysis; nested PCR; ss.
                                                                                                                                                                                                Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB
Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . This is the sequence of
the ligation of the two
(AAT09178-9). The ligated
PCR amplification with
                                                                                                                                                                                                                                      virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Length 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                   using polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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RESULT 9-
AAT11269
ID AAT1
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                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                     WO9535390-A1
                                                                                                                                                                                                                                                                                                                                                                                              2-1. The 5'-UTR includes several stem-loop sequences. The antisense RNA is useful for inhibiting expression of HCV structural genes and thereby inhibiting viral replication in vivo. The antisense therapy can be used in addition to conventional interferon treatment of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                              Synthetic
                                                                     Ligase dependent polymerase chain reaction; LD-PCR; probe; hybridisation; ligand binding pair; ligase; paramagnetic bead; primer; amplification; hepatitis; untranslated region; UTR; rRNA; ss.
                                                                                                                                                                                                                                                                                                                                                           Sequence 140 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a specifically claimed example of RNA that is complementary (i.e. antisense) to part of the 5'-untranslated ris complement of the hepatitis C virus genome sequence contained in clone and the hepatitis C virus genome sequence contained in clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus (HCV) anti:sense RNA - inhibits HCV structural gene expression in vivo for treatment of HCV infection
                                                                                                                      Hepatitis C virus specific ligated
                                                                                                                                                14-AUG-1996
                                                                                                                                                                         AAT09172
                                                                                                                                                                                                AAT09172 standard; DNA; 145
                                                                                                                                                                                                                                                                                                                                                                                    infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TOFU ) TONEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP07303485-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone 2-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; therapy; hepatitis C virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT11269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT11269 standard; RNA; 140
                                                                                                                                                                                                                                                                                                                       ьосат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996-035187/04
                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                   CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 9; 12pp; Japanese.
                                                                                                                                                                                                                                                             CGGUGUACUCACCGGUUCCGCAGACCACUAUGGC 113
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94JP-0124609
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                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partial 5'-UTR antisense RNA AS3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibition; info
                                                                                                                                                                                                                                                                                                                                                          A; 43 C;
                                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                          46 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                       No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV; 5'-untranslated region;
ection; treatment; stem-loop;
                                                                                                                      amplification sequence.
                                                                                                                                                                                                                                                                                                                                                          25 U; 0 other;
                                                                                                                                                                                                                                                                                                                                 17;
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u
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                 Length 140;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                           1;
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RESULT 11 ABK86834 ID ABK8

standard; DNA; 145

В S

72

CGGTGTACTCACCGGTTCCGCAGACCACTATGGC

۳,

RNA detection; ss. nucleic acid detection; infectious disease; hepatitis.

Hepatitis C virus ligated amplification sequence

24-SEP-2002 ABK86834; ABK86834

(first entry)

06-JUN-2002 WO200244339-A2 Hepatitis C virus.

01-DEC-2000; 2000US-0728265 03-DEC-2001; 2001WO-US45822

(ZHAN/) ZHANG D Y

28-DEC-1995

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Matches
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel method of detecting a target nucleic acid (TNA) sequence involves use of the ligase dependent polymerase chain reaction method (LD-PCR). In this method, two probes are provided. The first probe contains a region at the 5' end which is complementary and will hybriwith the TNA, the 3' end of the first probe is generic and is bound tone half of a ligand binding pair (LBP). The second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second probe contains a region at the 5' end which is complementary to a region in the TNA where the second problementary to a region in the TNA where the second problementary to a region in the TNA where the second problementary to a region in the TNA where the second problementary to a region in the TNA where the second problementary to a region in the TNA where the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second problementary the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region at the 5' end which is complementary to a region in the TNA which is immediately adjacent to the complementary region of the first probe. When the probes are bound to the TNA, they can be ligated together using a conventional ligase. The TNA: ligated probe complex can be isolated by binding the first probe to a paramagnetic bead to which is attached the second half of the LBP. The TNA can be dissociated from the ligated probe complex which can then be detected either by a label attached to the second probe, by using an external probe or by PCR using the ligated probes as a template.

The probes AAT(09170-1 are used to detect the presence of Hepatitis C region of the complex which can be detected either by a label attached to the second probe as a template.
                                                                                                                                                                                                                                                                                                                                                                                                                                  virus in a sample. This sequence results probes and contains sequence which is comphepatitis C virus 5' untranslated region. by PCR using the primers AATO9159-60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ligation dependent polymerase chain reaction infections pathogens and abnormal human genes
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 51; 100pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
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                                                                                                                                                                                                  Local
                                                                                                                                                ω
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                                                                                                                                                                                             Similarity
CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                             145
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0263937
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                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                        A; 40 C;
                                                                                                                                                                                        66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                0;
                                                                                                                                                                                             Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                        40 G;
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  results from the ligation
                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is complementary to a region of region. The sequence can be dete
                                                                                                                                                                                                                                                                                                                                             T; 0 other;
                                                                                                                                                                                                                                                   DΒ
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                                                                                                                                                                                                                                              17;
                                                 ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                              Length 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for the detection e.g. HIV and
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reaction method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detected
                                                                                                                                                Gaps
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RESULT 12
AAQ43062/c
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Best Local
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     (COMM-) COMMON
                               21-NOV-1991;
24-JUN-1992;
                                                                          20-NOV-1992;
                                                                                                     27-MAY-1993.
                                                                                                                              W09310239-A.
                                                                                                                                                            Hepatitis
                                                                                                                                                                                     Non-coding region; hepatitis; C virus; blood donor; type 2; type HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3
                                                                                                                                                                                                   Non-coding
                                                                                                                                                                                                                                                             23-SEP-1993
                                                                                                                                                                                                                                   -255 to
                                                                                                                                                                                                                                                                                         AAQ43062
                                                                                                                                                                                                                                                                                                              AAQ43062 standard; cDNA; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the target nucleic acid isolation procedure, which can be performed in microtubes, microchips or micro-well plates, if desired. The method also allows the direct detection of RNA by probe amplification without the need for DNA template production. The assembly of the amplifiable of a single mutation in a target. The method can be easily automated. The present sequence represents the nucleic acid detection method the present start is a single middle applification sequence used in an example of the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 145 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The method allows for rapid, sensitive and standardised detection and quantification of nucleic acids from pathogenic microorganisms from samples from patients with infectious diseases. The method simplifies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detecting a target nucleic acid in sample. Preferably, the method is useful for detecting and quantitating nucleic acids from pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid using a Capture/Amplification (C/A) probe and an amplification probe (A-probe), where C/A probe contains generic sequences and sequences complementary to trarget nucleic acid sequence, and also contains a ligand bound to the non-complementary sequence of probe; ligand is capable of forming an affinity pair with a ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting a target nucleic acid by a ramification extension amplification method, involves carrying out the steps of carcarrying out ligand-dependent amplification and detection of target nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BRAN/)
(HSUI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is capable of forming an affinity pair with a ligand binding coated on matrix. The method of the invention may be used for
                                                                                                                                                                                                                       62 portion of 5' non-coding region of HCV; K2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRANDWEIN
HSUIH T C
                                                                                                                                                                                                                                                                                                                                                                              CGGTGTACTCACCGGTTCCGCAGACCACTATGGC 105
                                                                                                                                                                                                                                                                                                                                                                                                CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Page 78; 160pp;
                                                                                                                                                          C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                       (first entry)
 SERVICES AGENCY
                          91GB-0024696
92GB-0013362
                                                                     92WO-GB02143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from samples from patients with infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 A; 40 C;
                                                                                                                                                                                  differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                           7.18;4 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hsuih TCH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 22;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel method for detecting target nucleic cation (C/A) probe and an amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 G; 36 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                               NS-3; core region; type 3; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 145; 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                          33
                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   steps of capturing, detection of the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PT XX PX
The sequences given region of hepatitis
                                        Disclosure; Fig 1;
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PI Chan S, Simmonds P, Yap PL;

XX DR. WPI; 1993-182554/22.

XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus for diagnosing and treating HCV infection, screening virus for diagnosing and treating HCV types

PT virus for diagnosing and treating HCV types

PT blood samples and identifying different HCV types

PT blood samples and identifying different HCV types

PS Disclosure; Fig 1; 120pp; English.

CC The sequences given in AAQ43058-75 show the -255 to -62 non-coding cregion of hepatitis C virus (HCV) samples from 18 blood donors and cother HCV varients. Analysis of this region revealed the existance of three distinct groups of they differing by 9-14% in nucleotide cc sequence. Two of the groups identified were similar to those of HCV a novel virus type 1 and 2, whilst the third appeared to represent the NS-5 region (see also AAR37923-26), showed a high degree of sequence CC diversity with type 3 being phylogenetically different to type 1 and 2. The same degree differentiation was noted in the NS-3 (see AAR37927-30) xx

Sequence 159 BP; 29 A; 49 C; 48 G; 33 T; 0 other;
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AAQ43066/c
ID AAQ43066 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 33
DNA encoding antigenic peptide(s) of new types of hepatitis virus - for diagnosing and treating HCV infection, screening blood samples and identifying different HCV types
                                                                   WPI; 1993-182554/22
                                                                                                Chan S,
                                                                                                                        (COMM-) COMMON SERVICES AGENCY
                                                                                                                                                        24-JUN-1992;
                                                                                                                                                                    21-NOV-1991;
                                                                                                                                                                                                20-NOV-1992;
                                                                                                                                                                                                                             27-MAY-1993.
                                                                                                                                                                                                                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                          W09310239-A
                                                                                                                                                                                                                                                                                                      Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3;
                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1993
                                                                                                                                                                                                                                                                                                                                                        -255 to -62
                                                                                                                                                                                                                                                                                                                                                                                                                AAQ43066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 CGGTGTACTCACCGGTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
33; Conser
                                                                                              Simmonds P,
                                                                                                                                                                                                                                                                                                                                                region of 5' non-coding region of HCV K2b-1
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                   91GB-0024696.
92GB-0013362.
                                                                                                                                                                                             92WO-GB02143.
                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
                                                                                            Yap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                         159
                                                                                            PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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                                                                                                                                                                                                                                                                                                       SS
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HCV varients.

in AAQ43058-75 show the -255 to -62 non-coding C virus (HCV) samples from 18 blood donors and Analysis of this region revealed the existance

120pp; English

닭 .Q

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RESULT 14
AAQ43069/c
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 Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                       The sequences given in AAQ43058-75 show the -255 to -62 non-coding region of hepatitis C virus (HCV) samples from 18 blood donors and other HCV varients. Analysis of this region revealed the existance of three distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of the groups identified were similar to those of HCV varients termed type 1 and 2, whilst the third appeared to represent a novel virus type. Comparison of other regions of the genome, eg. the NS-5 region (see also AAR37923-26), showed a high degree of sequence diversity with type 3 being phylogenetically different to type 1 and 2. The same degree differentiation was noted in the NS-3 (see AAR37927-30) and core region (see AAR37931) between type 3 and type 1 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                  Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of three distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of the groups identified were similar to those of HCV varients termed type 1 and 2, whilst the third appeared to represent a novel virus type. Comparison of other regions of the genome, eg. the NS-5 region (see also AAR37923-26), showed a high degree of sequence diversity with type 3 being phylogenetically different to type 1 and 2. The same degree differentiation was noted in the NS-3 (see AAR37927-30) and core region (see AAR37931) between type 3 and type 1 sequences.
                                                                                                                                                                                                                                                                                                                 DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for diagnosing and treating HCV infection, screening blood samples and identifying different HCV types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -255
                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-182554/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COMM-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-1991;
24-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ43069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ43069 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 159 BP; 30 A; 48 C; 47 G; 34 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                  တ
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33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMON SERVICES AGENCY.
                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                    Simmonds
66.7%; ilarity 97.1%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region of 5' non-coding region of HCV Pt-1
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                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91GB-0024696.
92GB-0013362.
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                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA;
                                                              A; 48 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                  PL;
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   0
 Score 22; DB 14;
Pred. No. 2.5;
0; Mismatches 0
                                                           50 G; 31 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 14;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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   0
                               Length 159;
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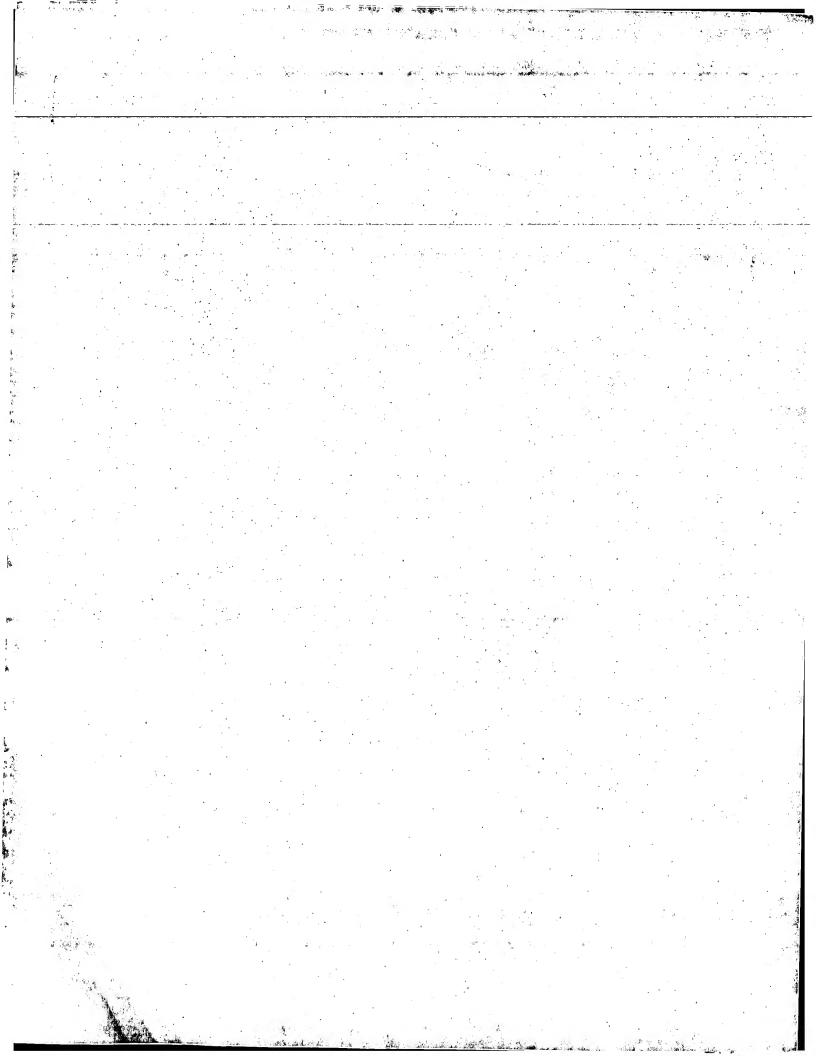
Gaps

Search completed: July 10, 2003, Job time: 70.6337 secs

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1:

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RESULT 15
AAQ43071/c
ID AAQ430
XX
AC AAQ430
XY
PT 23-SEP
XX
DT 23-SEP
XX
DE -255 t
XX
Non-co
KW Non-co
KW HCV; N
XX
OS Hepat1
XX
                                                                               Query Match
Best Local S
Matches 33
                                                                                                                                                                                               The sequences given in AAQ43058-75 show the -255 to -62 non-coding region of hepatitis C virus (HCV) samples from 18 blood donors and other HCV varients. Analysis of this region revealed the existance of three distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of the groups identified were similar to those of HCV varients termed type 1 and 2, whilst the third appeared to represent a novel virus type. Comparison of other regions of the genome, eg. the NS-5 region (see also AAR37923-26), showed a high degree of sequence diversity with type 3 being phylogenetically different to type 1 and 2. The same degree differentiation was noted in the NS-3 (see AAR37927-30) and core region (see AAR37931) between type 3 and type 1 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding antigenic peptide(s) of new types of hepatitis virus - for diagnosing and treating HCV infection, screening blood samples and identifying different HCV types
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-182554/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-1993
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                                                                                                                                                              Sequence
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24-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9310239-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV; NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 to -62
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    84
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                                                                                                   Similarity
159 BP; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
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                                                                                 Conservative
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92GB-0013362.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA;
                                                                                                                                                                A; 49 C;
                                                                                                 66.7%;
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                                                                                 0
                                                                                                   Score 22;
Pred. No.
                                                                                                                                                                50 G;
                                                                               Mismatches
                                                                                                                                                                30 T; 0 other;
                                                                                                                      DB 14; Length 159;
    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                   0
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                                                                                   Indels
                                                                                   ۲.
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on:
                                                                                                                                                                                                                                                                                                                        score greater than or equal to the score and is derived by analysis of the total
                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                         Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2185239 seqs, 1125999159 residues
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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  ABA96260
ABA96259
AAQ32444
                                                                   ABN79970
ABL46275
AAZ08979
AAX24834
AAX24835
AAZ57773
                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (without alignments)
1067.241 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                             score distribution.
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L/NA1990.DAT:*
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Infectious hepatit
Infectious hepatit
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
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Hepatitis C virus
Hepatitis C virus
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241 2441 2441 2441 2441 2441 2441 2441
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0
483 587 703 773 773 773 770 780 780 780 780 780 780 780 780 780
13 21 21 21 21 21 21 21 17 17 13 16
AAQ32445 AAZ57395 AAQ54921 AAZ57396 AAA08097 ABL52861 AAZ57789 AAT28348 AAQ32451 AAQ64913 AAQ64913
HCV core-envelope Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus Hepatitis C virus

#### ALIGNMENTS

ABN79970 ID ABN79970; XX AC ABN79970; XX AC ABN79970; XX DT 15-JUL-2002 (first entry) XX DE Hepatitis C virus 5' untranslated region genotype 1b. XX Example nucleotide polymorphism; nucleic acid typing; hepatitis C KW tissue typing; untranslated region; UTR; ds; HCV. XX OS Hepatitis C virus. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0200220837-A2. XX PN W0300220837-A2. XX PN W03002208																								
BN79970; BN79970;  5-JUL-2002 (first entry)  lepatitis C virus 5' untranslated region genotype 1b.  lingle nucleotide polymorphism; nucleic acid typing; hepatitis visue typing; untranslated region; UTR; ds; HCV.  lepatitis C virus.  10200220837-A2.  4-MAR-2002.  0-SEP-2001; 2001WO-GB04042.  18-SEP-2000; 2000GB-0022069.  PYRO-) PPROSEQUENCING AB. STRD ) UNIV LELAND STANFORD JUNIOR.  GARD) GARDNER R.  Conaghi M, Ekstroem B, Pourmand N;  PI; 2002-393849/42.	44			 _	_	_	××			XX		××		XX						XX		ID.	ABN799	RESULT
Ω .		PI; 2002-393849/42.	EKSTroem B,		_	PYRO-) PYROSEQUENCING AB.		)8-SEP-2000; 2000GB-0022069.	0-SEP-2001; 2001WO-GB04042.		4-MAR-2002.		10200220837-A2	-	lepatitis C virus.	issue typing; untranslated region; UTR; ds; HCV.	single nucleotide polymorphism; nucleic acid typing; hepatitis C	epatitis C virus 5' untranslated region genotype 1b.			BN79970;	BN79970 standard; DNA; 305 BP.	70	

virus;

PX

Typing nucleic acid for obtaining information about several variable

sites primer

primer extension reactions, incorporation -

involves simultaneously

ly or sequentially performing two or more and determining the pattern of nucleotide

pattern of nucleotide

le 1; Fig 2;

86pp;

English

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RESULT 2
ABL46275
ID ABL4
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      (THIR-)
                                    17-JUN-2000;
                          15-JUN-2001;
                                                              15-JUN-2001;
                                                                                     27-DEC-2001.
                                                                                                             WO200198537-A2.
                                                                                                                                     Hepatitis
                                                                                                                                                                      characterisation;
                                                                                                                                                                                                 Hepatitis C virus subtype 1a mRNA sequence SEQ ID NO:242.
                                                                                                                                                              gene;
                                                                                                                                                                                      Nucleic
                                                                                                                                                                                                                                  26-APR-2002
                                                                                                                                                                                                                                                           ABL4627
                                                                                                                                                                                                                                                                                   ABL46275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sites, preferably nucleic acid molecules containing three or more variable sites are typed, where three or more primer extension reactions are performed. The method is also useful for diagnosis of pathological molecule(s). The method is presence of specific nucleic acid molecule(s). The methods are particularly suited for identifying of polymorphisms, tissue typing or in clinical applications. The sequence of polymorphisms, tissue typing or in clinical applications. The sequence genotype, amplified in the invention to type HCV-positive sera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      typing sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  about several variable sites within target nucleic acid, or ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                              SS
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                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241;
THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                              acid accessible hybridisation
                                                                                                                                     C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                standard; RNA; 328
                                                                                                                                                                                                                                                                                                                                            C 266
                                                                                                                                                                                                                                                                                                                                                                  C 241
                                                                                                                                                                                                                                                                                                                                                                                                       TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTCCTTTCTTGGATCÅACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 BP;
                         2000US-212308P.
2001US-0212308.
                                                           2001WO-US19401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or more nucleic acid molecules containing two or more variable ferably nucleic acid molecules containing two or more variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 241; DB 24; 100.0%; Pred. No. 2.9e-62; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to
                                                                                                                                                                    identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 A; 87 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a novel
                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 G; 64 T; 0 other;
                                                                                                                                                                    nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method for obtaining typing information hin target nucleic acid, or typing one o
                                                                                                                                                                         site; detection; hybridisation;
                                                                                                                                                               acid structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                diagnosis;
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                                                                                                                                                                                                                                                                                                                                                secondary structure. The method comprises amplifying a target nucleic that form an extension product are identified as the oligonucleotides which can interact with the folded target nucleic acid. Oligonucleotides from the present invention can be used in novel detection methods for of pathogenic organisms (e.g. HIV). The method allows the ability to rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                  Sequence 328 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for identifying oligonucleotides with desired hybridisation properties to nucleic acid targets containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 48; Fig 74; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying oligonucleotides hybridizing to nucleic acids containing secondary structure, useful in clinical diagnosts, comprises identifying primers that interact with the target to form an extension product under amplification conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-049698/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyamichev
241
                 230 UGCUAGCCGAGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUG
                                             181 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                         170
                                                                                            121 GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTTGGGCGTGCCCCCGGGAGAC
                                                                                                                                                    110
                                                                                                                                                                                                             50
                                                                                                                                                                                                                                                                       190;
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C 241
                                                                                                                                                                                                                                                                                      Similarity
                                                                             CCCGGGAGAGCCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACC
                                                                                                                                                        CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                                                                                                                       GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allawi
                                                                                                                                                                                                                                                                                                                              63 A; 95 C;
                                                                                                                                                                                                                                       100.0%; Pred. No. 78.8%; Pred. No. 178.8%; Pred. No. 178.7%; Mismatches
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                                                                                                                                                                                                                                                                                                                         102 G; 68 U; 0 other;
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                                                                                                                                                                                                                                                                                                DВ
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X S X
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28-JAN-1999;
                                                                                Genetic vaccine; immunisation; humoral response; non-structural protein; NS protein; antigen; ds.
                                           WO9938880-A1
                                                               Hepatitis C
                                                                                                                   Hepatitis C
                                                                                                                                        02-NOV-1999
                                                                                                                                                           AAZ08979;
                                                                                                                                                                               AAZ08979
                                                                                                                                                                             standard; DNA;
                                                              virus
                                                                                                                  virus 5'
                                                                                                                                    (first entry)
  99WO-US01823
                                                                                                            UTR used as promoter for a
                                                                                                                                                                             341
                                                                                                                                                                             ВР
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HCV genetic vaccine. cellular response;

30-JAN-1998;

98US-0073156

RESULT 3

В

290

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290

240 289

229 180 169 120 109 60. 0

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Best Local (
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructs expressing one NS protein were found to elicit strong antigen specific immune responses in both arms of the immune system. This demonstrated that the NS proteins are better antigens for stimulating humoral immune responses as compared with previous studies using the HCV core structural protein. The genetic vaccine is useful for inducing an immune response (cellular or humoral) against hepatitis C virus in a human uninfected by the virus, and for immunising a human susceptible to hepatitis C viral infection by inducing an immune response. The composition is also useful for treating a human infected with hepatitis C virus, by induction of an immune response. The advantage of this method of immunisation compared with immunisations with soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NS) proteins. The HCV genome encodes three NS proteins: NS3, a serine protease/viral helicase; NS4; and NS5, the viral RNA-dependent RNA polymerase. In HCV infection, these and other virally encoded proteins are produced by proteolytic processing of a precursor polypeptide. However, for use in a genetic vaccine, the sequences coding for NS proteins had to be engineered so that each NS sequence had its own initiation and stop codons. Restriction sites were also engineered into the gene fragments to aid subcloning. The gene fragments were isolated and mutated using PCR. The NS3 coding sequence was modified using PCR primers AAZ08981 and AAZ08985, and the NS5 coding sequence modified using AAZ08984 and AAZ08985. Studies in munised with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the hepatitis C virus (HCV) 5' untranslated region (5' UTR). This is preferred for use as a promoter in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant proteins or peptides, is the ability to induce a strong inflammatory CD4+ T cell response as well as cytotoxic T cell activity. In addition, the new recombinant genetic vaccine is more suitable for immunisation, unlike synthetic peptides which only have a limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant DNA vaccine against hepatitis C. The genetic vaccine comprises regulatory elements capable of directing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine comprises regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                               241 C 241
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                                                                  TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                           GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTTGGGCGTGCCCCCCGCGAGAC
                                                                                                                                                                                                             CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 10-11; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         against the virus
                                                                                                                                        GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitopes available for
 308
                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                          63 A; 103 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and one or more HCV non-structural
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                    Score 241; DB 20; Pred. No. 3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                          106 G;
                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulation
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                                                                                                                                                                                                                                                                                                                                                                                                                           69 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the host
                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           response
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RESULT 4
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Matches
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                The present sequence comprises a consensus of the 5' untranslated regions (5'UTR) of hepatitis C virus (HCV) infectious clones of genotype 1a (pCV-H77C, see AAX24836) and 1b (pCV-41416S, see AAX24835). The invention discloses nucleic acid sequences (see AAX24832-33 and AAX24843) which encode infectious HCV viruses, and the use of these sequences, and polypeptides (see AAW98020-22) encoded by them, in the development of vaccines and diagnostics for HCV and in the development of screening assays for the identification of antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated hepatitis C virus nucleic acids - used to deveproducts for the diagnosis, prevention and treatment of HCV infections and for developing screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-132252/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening; assay; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX24834 standard; DNA;
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 11; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1998;
18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV; infectious clone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infectious hepatitis C virus genotype Ta/1b
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                                                                                                                                                                                                                                                                 Local Similarity
 241
                             248
                                                                                                               121
                                                        181
                                                                                    188
                                                                                                                                            128
                                                                                                                                                                     61
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    ဂ
                                           TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                 GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
                                                                                                                                                         CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                                                                                               341
                                                                                                                                            CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                                                                                                                         GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emerson SU,
                             TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                    GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
 241
                                                                                                                                                                                                                                                                                                                                          HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                     '100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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97US-0053062.
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                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                           A; 103 C; 106 G; 69 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purcell RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; diagnosis; therapy; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                     Score 241; DB 2
Pred. No. 3e-62;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yanagi M;
                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'UTR consensus
                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to develop
                                                                                                                                                                                                                                                                               Length 341;
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                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                   Sequence 341 BP;
                                                                                                                                                                                                                                                                                                                                                            The invention discloses nucleic acid sequences (see AAX24834) produced. AAX24843) which encode infectious HCV viruses, and the use of these sequences, and polypeptides (see AAW98020-22) encoded by them, in the development of vaccines and diagnostics for HCV and in the development of screening assays for the identification of antiviral agents for HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                  of hepatitis C virus (HCV) genotype 1b infectious clone pCV-J4L6 This has been compared with the 5'UTR of genotype 1a infectious clone pCV-H77C (see AAX24836) and a consensus (see AAX24834) pcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence comprises the 5' untranslated region of hepatitis C virus (HCV) genotype 1b infectious clone po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated hepatitis C virus nucleic acids - used to products for the diagnosis, prevention and treatment o infections and for developing screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-132252/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-1998; .
18-JUL-1997; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV; infectious clone; infection; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN <del>|</del> 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9904008-A2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX24835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infectious hepatitis 'C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN 1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX24835;
                           241
308 C
                                                      248
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                                                                                                            188
                                                                                                                                                                                                                                                                           Similarity 100.
                                          TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                     TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                GGGTCCTTTCTTGGATCAACCCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCCGCGAGAC
                                                                                                               GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCGGGAGAC
                                                                                                                                                    7; Fig 11;
                                                                                                                                                                                                          GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US DEPT HEALTH & HUMAN SERVICES.
308
                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0014416.
97US-0053062.
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                                                                                                                                                                                                                                                                                                                              63 A; 103 C; 106 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiviral; virucide;
                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purcell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus genotype 1b 5'UTR.
                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                     Score 241; DB 20;
Pred. No. 3e-62;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yanagi M;
                                                                                                                                                                                                                                                                                                                          69 T; 0.other;
                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                               Length 341;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to develop
of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              on (5'UTR)
pCV-J4L6S.
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                                            307
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181 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG

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AAZ57773/c
ID AAZ57773 standard; E
XX
AC AAZ57773;
XX
CDT 05-APR-2000 (first
XX
DT 05-APR-2000 (first
XX
                                                                                                                                                                                                                                                                             PTXX
                                                                                                                                                                                                          Matches 241;
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             vector comprising a nucleotide sequence, which is transcribed in an animal cell to generate an antisense oligonucleotide. The oligonucleotides have virucide, hepatotropic and anti-inflammatory activity, and are useful for treating HCV infection by inhibiting translation of type I-V HCV RNA. Hepatitis C virus is a positive strand RNA virus, and is the major causative agent of post-transfusion hepatitis. Persistent HCV infection can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma.
                                                                                                                                                                                                                                                                   Sequence 342 BP; 69 A; 106 C; 103 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is an antisense oligonucleotide that hybridises Hepatitis C virus (HCV) RNA, under physiological conditions. Tinvention relates to HCV antisense oligonucleotides, and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide to Hepatitis C virus RNA, useful Hepatitis C virus infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-104900/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis_C virus;
anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moradpour D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6001990-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C
155 GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
                                             121
                                                                            215
                                                                                                                                             275
                                                                                61 CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGGAATTGCCAGGACGACC
                                                                                                                                                                              \vdash
                                                                                                                               GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCT
                   GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
                                                                CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCCAGGACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Column 31; 31pp; English.
                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus antisense inhibitor oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wands JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0240382,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0474700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV; antisense oligonucleotide; hepatotropic; translation inhibition; HCV infection; virucio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakita
                                                                                                                                                                                                        0;
                                                                                                                                                                                                   Score 241; DB 21;
Pred. No. 3e-62;
Wismatches 0;
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tropic; ss; virucide.
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RESULT 8
ABA96259
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AC ABA9
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 241
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a vector for analysing RNA virus replication, comprising DNA encoding RNA virus-derived RNA dependent RNA polymerase (ABA96256-ABA96351), for evaluation of RNA virus-derived RNA dependent RNA dependent RNA polymerase activity by studying interaction between viral proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TOKM-)
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 55; 66pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector for analysing RNA virus replication, virus-derived RNA dependent RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kohara M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2000; 2000JP-0142451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200188161-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA96260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA96260 standard; DNA;
           ABA96259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2002
                                ABA96259 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-114236/15
                                                                                                                                                                                                                                                                                                                                                                        factors and
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                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                        241;
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CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                               CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTTGCCAGGACGACG
                                                                                                                                                                                                                                                                         C 320
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                                                                                                                                                                                                                                                                                                                                                 393 BP; 83 A; 115 C;
                                                                                                                                                     TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                                        GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCCGTGCCCCCGCGAGAC
                                                                                                                                                                                                                   CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                                                                                                                                                             GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
                                                                                                                                TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuzaki J,
                                                                                                                                                                                                                                                                                                      100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                   the level of expression of reporter genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA polymerase encoding polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA polymerase; RNA virus replication;
                                DNA;
                                412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamoto K,
                                                                                                                                                                                                                                                                                                       0
                                ВP
                                                                                                                                                                                                                                                                                                      Score 241; DB 24; Pred. No. 3.1e-62; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 120 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDICAL
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RESULT 9
AAQ32444
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DT 26-A
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KW HC;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 412 BP; 92 A; 119 C; 120 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a vector for analysing RNA virus replication, comprising DNA encoding RNA virus-derived RNA dependent RNA polymerase (ABA96256-ABA96261), for evaluation of RNA virus-derived RNA dependent RNA polymerase activity by studying interaction between viral proteins host factors and the level of expression of reporter genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector for analysing RNA virus replication, virus-derived RNA dependent RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2000; 2000JP-0142451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200188161-A1
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                                                                     26-APR-1993
                                                                                               AAQ32444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-114236/15
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                                         HCV core-envelope clone N1-1.
                                                                                                                           AAQ32444 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUS ) CHUGAI SEIYAKU
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                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                            C 241
                                                                                                                                                                                                                                                                                                                             GGGTCCTTTCTTGGATCAACCCGCTCAATGCCCTGGAGATTTGGGCCGTGCCCCCCGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                                                                                                                                                                             CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                                                                                                                                                                          TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 55; 66pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsuzaki J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus RNA polymerase encoding polynucleotide
                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-JP04033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okamoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 241; DB 24; Pred. No. 3:1e-62; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA virus replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Katsume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contains DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                    240
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Clone; polypeptide; core-envelope; region; Hepatitis HC; cDNA; transcriptase; primer; allele; diagnostic;

C; Virus; HCV; antibody;

control;

proteolytic

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Best Local
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                 RNA sequences were converted into CDNA using transcriptase in the presence of one of the primer sequences given in AAQ32340-46. The CDNA sequences isolated represent different alleles of the same region of the HCV|gene. The entire HCV gene (see AAQ32436) is useful in the development of a diagnostic method which is more accurate and effective than conventional ones, in the detection of antibodies raised against a wide range of HCVs which have been hardly detected before. The complete gene may be used in an in vitro screening system for a substance capable of specifically supressing or controlling a proteolytic processing of a precursor polypeptide of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequences given in AAQ32438-39 and AAQ32444-53 are various clones which encode the polypeptide core-envelope region of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptage in the
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 33; Page 74; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosing and vaccinating against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hepatitis C virus gene and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-
12-JUL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Teranishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP518313-A.
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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-1992.
                                                                                                                                                                                                                                                                                                                                 Local Similarity
 284
                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1992-417213/51.
DB; AAR29534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1991;
C 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1992;
                              C 241
                                                                                                                                                                           CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                TECTAGCCGAGTAGTGTTEGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                     GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGGGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             z
                                                  TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                               GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
                                                                                                                                                                                                                                         GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1991;
                                                                                                                                                                                                                                                                                                                                                                                  483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1991;
                                                                                                                                                                                                                                                             GCAGAAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Honda Y,
                                                                                                                                                                                                                                                                                                                                                                        BP; 102 A; 141 C; 146 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
92JP-0099957.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 318..482
                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakami T,
                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                            Score 241; DB 13; Pred. No. 3.2e-62; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 processing; precursor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded protein - used for hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi K;
                                                                                                                                                                                                                                                                                                                                          Length 483;
                                                                                                                                                                                                                                                                                                            Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The cDNA
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61 CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC 120

GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCT GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCT

103 60 Best Loc Matches

Local

Similarity

100.0%;

Conservative

0

Score 241; DB 13; Pred. No. 3.2e-62; ; Mismatches 0;

Length Indels

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AAQ32445
         Sequence 483
                                before. The complete gene may be used in an in vitro screening system for a substance capable of specifically supressing or controlling a proteolytic processing of a precursor polypeptide of HCV.
                                                                                   RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32540-46. The sequences isolated represent different alleles of the same region of the HCV gene. The entire HCV gene (see AAQ32436) is useful in the development of a diagnostic method which is more accurate and raised against a wide range of HCVs which have been hardly detected raised against a wide range of HCVs which have been hardly detected
                                                                           before.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                                                                                                                                                                                                      which encode the polypeptide core-envelope region of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptage in the
                                                                                                                                                                                                                                                     The sequences given in AAQ32438-39 and AAQ32444-53 are which encode the polypeptide core-envelope region of the
                                                                                                                                                                                                                                                                                                                  Claim 33;
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-417213/51.
P-PSDB; AAR29535.
                                                                                                                                                                                                                                                                                                                                              New nepatitis C virus gene and its diagnosing and vaccinating against
                                                                                                                                                                                                                                                                                                                                                                   New hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone; polypeptide; core-envelope; region; Hepatitis C; HC; cDNA; transcriptase; primer; allele; diagnostic; ant supress; control; proteolytic processing; precursor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ32445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ32445 standard; DNA; 483
       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0287008.
91JP-0332329.
92JP-0099957.
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91JP-0172794
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   102 A; 141 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 318..482
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                                                                                                                                                                                                                                                                                                          305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakami T,
146 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          encoded protein - hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi
                                                                                                                                                                                                                                                                                                                                          infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s C; Virus; antibody;
                                                                                                                                                                                                                                                                                                                                                               used
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                                                                                                                                                                                                                                                                      various
                                                                                                                                                                                                                                               arious clones
Hepatitis C
                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                             The cDNA
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RESULT 11
AAZ57395
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                                                                                  Query Match
Best Local
                                                                      Matches
                                                                                                                                                                The present invention describes a vector comprising a cDNA encoding an RNA virus gene, constructed to ensure the exact and homogeneous transcription of both terminals of the RNA virus gene. Also described is a method for screening drugs for inhibiting the replication of RNA virus by using the RNA viral infection model animal, particularly one with hepatitis C viral infection. The vector is useful in clarifying the mechanism of RNA viral replication, onset of RNA viral infection, and developing remedies and therapeutics for RNA viral infections, particularly of a hepatitis C virus. The present sequence represents
                                                                                                                                                                                                                                                                                                              Vectors expressing full-length gene of RNA viruses, useful clarifying mechanisms of RNA viral replication, infection, developing remedies and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis
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                                                                                                                    Sequence 587
                                                                                                                                                                                                                                                                                        Example 1; Page 35; 46pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                            (CHUS ) CHUGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus;
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                                                                                 Local Similarity
                                                                                                                                                       DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104
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 61
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CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
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                     GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
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                                                                      Conservative
                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                            SEIYAKU
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                                                                                                                   122 A; 178 C; 178 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA
                                                                                                                                                       hepatitis C virus
                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                      Taira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus; replication; viral infection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                    Score 241; DB 21;
Pred. No. 3.3e-62;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                     Matsuzaki J,
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RESULT 12
AAQ44921
ID AAQ44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                 Oligonucleotides which are complementary to part of the hepatitis virus genomic or messenger RNA are claimed. Preferred antisense oligonucleotides are complementary to RNA comprising regions of the 5'-UTR, esp. the 5'end hairpin loop, 5'end 6bp repeat and 5'end untranslated region.
                                                                                                                                                                                            (KAGA )
(ISIS-)
(MOCH )
                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; non-A, non-B hepatitis antisense oligonucleotide; translation inhibit 5'-untranslated region; 5'-UTR; hybridisation
                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                5'UTR
                                                                               Disclosure;
                                                                                                   diseases
                                                                                                            Anti:sense oligo:nucleotide(s) complementary to hepatitis C genome - useful for inhibiting HCV replication, to treat rel
                                                                                                                                                                                                                                     10-SEP-1992;
14-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ44921 standard;
                                                                                                                                           WPI; 1994-101217/12.
                                                                                                                                                               Hoshiko
                                                                                                                                                                          Anderson
                                                                                                                                                                                                                                                                    10-SEP-1993;
                                                                                                                                                                                                                                                                                       17-MAR-1994
                                                                                                                                                                                                                                                                                                          WO9405813-A.
                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus 5'-untranslated region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ44921;
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                                                                                                                                                                                                      CHEMO SERO THERAPEUTIC ISIS PHARM INC.
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                                                                              Fig 1; 91pp; English.
                                                                                                                                                               Nakatake
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93JP-0087195
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/note= "partial coding
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H, Nishihara
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de; translation inhibition; therapy;
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Nozaki
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Query Match

Sequence

989

BP;

129 A; 214 C;

221 G; 1 T; 0

100.0%;

Score

241;

DB 15; other;

Length

686;

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Matches
                                                                                                 The present invention describes a vector comprising a cDNA encoding an RNA virus gene, constructed to ensure the exact and homogeneous transcription of both terminals of the RNA virus gene. Also described is a method for screening drugs for inhibiting the replication of RNA virus by using the RNA viral infection model animal, particularly one with hepatitis C viral infection. The vector is useful in clarifying the mechanism of RNA viral replication, onset of RNA viral infection,
                                                                                                                                                                                                                              Vectors exp
                                       Sequence
                                                                                           and developing
                                                                                  particularly
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                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
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                                                                        sequence
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                                                                                                                                                                                                            expressing full-length gene of RNA viruses, usefuling mechanisms of RNA viral replication, infection, ing remedies and therapeutics
                                                                                                                                                                                             1: Page 35-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                              ng remedies and therapeutics for RNA viral infections, of a hepatitis C virus. The present sequence represents ce from hepatitis C virus from an example of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus DNA sequence SEQ ID NO:3.
                                     BP; 151
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                                     A; 211 C;
               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         virus;
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               Score
                                  213 G;
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                                  128 T;
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Claim 18; Page 82-84;

94pp;

Japanese.

The present invention describes an oligonucleotide sequence which potentiates the expression of a useful gene when incorporated in a gene expression vector, where the oligonucleotide sequence consists of the 5'-non-translated region (5'UTR) of a viral genome or its fragment or modified form. The 5'UTR sequence is useful in screening potential initiation factors of interaction with the viral IRES or

screening

Nucleic acid sequence which potentiates gene expression and contains 5'-non-translated region of a viral genome is incorporated in vector for improving the expression of a useful gene

vectors

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 P-PSDB;
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                                                                                                                                              WO200012691-A1
                                                                                                                                                                                                                   Key
5'UTR
                                                      (FUSO ) FUSO PHARM IND
                                                                            27-AUG-1998;
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                                                                                                   08.-JUL-1999;
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                                                                                                                                                                                                                                                                          Hepatitis C virus; gene expression; i
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2000-237867/20
DB; AAY82358.
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                               Yoshida . H,
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                                                                                                                                                                                                                                                   virus.
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342..713
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Mismatches 0;
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Best Local Similarity
Matches 241; Conserv
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                   The present invention relates to a method for titration of hepatitis C virus in serum. The method comprises quantitive and competitive polymerase.chain reaction (PCR). The present sequence, a 5 untranslaregion (UTR) of Hepatitis C virus, was used to illustrate the invent:
                                                                                                        Titration of hepatitis C-Virus in serum employing quantitive competitive polymerase reaction - No Abstract \,
                                                                                                                                               WPI;
                                                                                                                                                                        Choo
                                                                                                                                                                                                                                                                                                                                                              Titration; quantitive PCR; competitive PCR;
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                                                                                 Disclosure; Fig 1; 12pp; Korean.
                                                                                                                                                                                                                         31-AUG-1994;
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 A52660/c LOCUS DEFINITION ACCESSION VERSION		C 44	44	. 4.	-ω	w w	w		w w	ωu	ພພ	N	מינ	NN	N	งผ	2 -	, <sub>1</sub>		<u>,</u>		ے ب	ــر د			ი ი თ თ				
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,M., Carloni,G PROPAGATE THE CELL CULTURES 5 15-AUG-1996;	36 bp DNA 1t WO9624662.	ALIGNMENTS	HCU56545 HCU56546	654	65.		HCU56538	HCU56537	HCU56535	HCU56534	HCU56532	HCU56530	HCU56529	HCU56527	HCU56525 HCU56526	HCU56524	HPCEB9	HPCEB/		HPCEB16	EB1	HPCEB11	HPCEB1	HPCCHA6	S72378	нрссна10	HPCCHA12	AX003356	291 0335	A52660	ID
., Ponzetto,A. and Iacovacci,S. HEPATITIS C VIRUS (HCV) IN NON AND PRODUCTS THEREOF	NA linear · PAT 12-DEC-1997		U56545 Hepatitis C U56546 Hepatitis C	Hepatitis	Hepatitis	Hepatitis	Hepatitis	Hepatitis	Hepat Hepat	Hepatitis	Hepatitis	Hepatitis	Hepatitis	Hepatitis	Hepatitis .	Hepatitis	Hepatitis	Hepatitis	Hepatitis	Hepatitis Hepatitis	Hepatitis	Hepatitis	D10114 Hepatitis C	Hepatitis	(5′ regio	M74252 Hepatitis	M74254 Hepatitis C M74255 Hepatitis C	003356 Sequence	Sequence	2660 Sequence 5	Description

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Sequence 6 from Patent WO9928503
AX003355
                                                                         PRIMI DANIELE (IT);
                                                                   ethods of detecting polynucleotide analytes
Patent: WO 9928503-A 6 10-JUN-1999;
PRIMI DANIELE (IT): MANTERO GIOVANNI (IT)
                                                                                                         Primi, D. and Mantero, G.
                                                                                                                                        Viruses; ssRNA positive-strand viruses,
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Hepatitis C virus
                                                                                                                                                                                         AX003355.1 GI:9927160
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                                                                                                                                  lepacivirus
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Other publication AU 1822195 960827.
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                    1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
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                                                                                                                                                                                          Cha, T.-A., Kolberg, J., Irvine, B., Stempie
Choo, Q.-L., Houghton, M., Kuo, G., Han, J.H.
                                                                                                                                                                                                                                      Hepatitis C virus cDNA to genomic RNA.
Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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                                                                                                                                                                         Use of a signature nucleotide the detection of viral RNA in
                                                                                                                                                            Unpublished
                                                                                                                                                                                                                               Hepacivirus.
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                                                                                                                                                                                                                                                                                                    Hepatitis C virus isolate M74254
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97.1%;
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97.1%;
                                          Score 22; DB
Pred. No. 4.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 6; L
Pred. No. 5.2e+02;
0; Mismatches 0;
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Pred.
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te I24 genome, s
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                                                                                                                                                                               sequence of
                                                                                                                                                                      human serum
                                     DB 1.,
4.8e+02;
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5.2e+02;
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                                           Indels
                                                                                                                                                                                                                                      DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stage;
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                                          1;
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30

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RESULT
E10301
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ORGANISM
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DEFINITION
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HPCCHA10/c
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HPCCHA13/c
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Best Local S
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                     E10301
Anti-sense
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M74255
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virus.
E10301
                                                                                                                                                                                                                                                            Cha.T.-A., Kolberg,J., Irvine,B.,
Choo,Q.-L., Houghton,M., Kuo,G., I
Use of a signature nucleotide seq
the detection of viral RNA in huma
                                                                                                                                                                                                                                                                                                                            Hepatitis C virus cDNA to genomic RNA.
Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                  Map
                                                                                                                                                                                                                                                  Unpublished (1991)
                                                                                                                                                                                                                                                                                             Cha, T.-A., Kolberg, J.,
                                                                                                                                                                                                                                                                                                                                                                             M74252.1 GI:329741
                                                                                                                                                                                                                                                                                                                                                                                                         HPCCHA10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M74255.1 GI:329744
                                                                                                                                                                                                                                                                                                                   depacivirus.
                                                                                                                                                Similarity
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                                                                                         CGGTGTACTCACCGGTTCCGCAGACCACTATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position 108.
                                                                                                                                                                                  position 99.
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                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hepatitis C
/db_xref="taxon:11103"
40 c 33 g
                                                                                                                                                                                          /organism="Hepatitis C
/db_xref="taxon:11103"
42 c 37 g
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                       RNA
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97.1%;
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97.1%;
                     against
                                                                                                                                              Score 22;
Pred. No.
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Pred.
                     140 bp RNA linear partial sequence of 5'UTR
                                                                                                                                                                                                                                                                                                                                                   to genomic RNA
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G., Han, J.H. and I
sequence of the
human serum and
                                                                                                                                                                                                                                                            sequence of human serum
                                                                                                                                 Db _
. 4.8e+02;
0;
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4.8e+02;
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                               PAT 29-SEP-1997
                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                               Flaviviridae;
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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ORGANISM
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S72378/c
  FEATURES
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AUTHORS
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VERSION
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REMARK
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Best Local
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{5' re
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Funahashi, S. and Hasegawa, A.
HCV ANTI-SENSE RNA, WANIFESTATION VECTOR CONTAINING THERAPEUTIC AGENT FOR HCV-INVOLVED DISEASE CONTAINING
          GenBank staff at the National Library of Medicine created thientry [NCBI gibbsq 152236] from the original journal article. This sequence comes from Fig. 1.
                                                                       Sullivan, D.E. and Gerber, M.A. Conservation of hepatitis C virus hepatocellular carcinoma and the shepatology 19 (3), 551-553 (1994)
                                                                                                                                                            Hepatitis C virus host-human liver Hepatitis C virus
                                                                                                                                                                                                                      [5' region]
142 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
                                                 8119678
                                                                                                                                     Hepacivirus
                                                                                                                                                 Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent:
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                                                                                                                                                                                                                                                                                                         (bases 1 to 142)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1994 JP 1994124609
FUNAHSHI SHINICHI, HASEGAWA AKIRA
FUNAHS/09, ASIK31/70, ASIK31/70, C07H21/04;
strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Artificial sequences
JP 1995303485-A/2
21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        None
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hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/db_xref="taxon:32644"
43 c 46 g 2
Location/Qualifiers
                                                                                                                                                                                                 GI:632885
                                                                                                                                                                                                                                  [hepatitis
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97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yes;
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                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note='Anti-sense RNA of 5'UTR of hepatitis C virus'.
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Pred.
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No.
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4.7e+02;
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                                                                                  s 5' untranslated
surrounding liver
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man liver,
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/organism="Hepatitis C /db\_xref="taxon:11103"

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REFERENCE
AUTHORS
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S75838/c
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ORIGIN
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ACCESSION
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HPCCHA6/c
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REMARK
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Best Local
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                                                       GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 161727] from the original journal article. This sequence comes from Fig. 2.
                                                                                                                                                                                                                                                                                        NS-5 {
A1 8,
S75838
                                                                                                                                                                                                                                     Hepatitis C virus type 1 host=human.
Hepatitis C virus type 1
                                                                                                                                                                                                                                                                            $75838.1 GI:913831
                                                                                                                                                                   erotto,M., Pontisso,P., Giostra,F., Francesconi,R., Mailardini,G., Lenzi,M., Tisminetzky,S., Bianchi,F.B.,
                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                               S75838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cha,T.-A., Kolberg,J., Irvine,B.,
Choo,Q.-L., Houghton,M., Kuo,G., I
Use of a signature nucleotide sequence of a signature nucleotide sequence the detection of viral RNA in humo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
M74248
M74248.1 GI:3297
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33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1991)
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                                                                                                                                     nti-LKM-1 autoantibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepacivirus.
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                                                                                                               Hepatol. 21 (2),
)81562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                    (bases 1 to 148)
                                                                                                                                              lysis of the hepatitis C virus genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 148)
                                                                                                                                                                                                                                                                                                 148 bp RNA linear (5' untranslated region) [hepatitis C virus 1, host-human, Genomic RNA, 148 nt]
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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             /organism="Hepatitis C virus
/isolate="Al 8"
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hepatitis C virus"
/db_xref="taxon:11103"
47 C 44 g 30 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 bp ss-RNA
isolate NB011 genome
                                                                                                                       273-276 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
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Pred. No.
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of human serum
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4.7e+02;
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                      type
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                     no DNA stage; Flaviviridae;
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                                                                                                                                                in patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 148;
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the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Urdea, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis C virus for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beall, E.,
                                                                                                                                                                                                                                                                                                         HCV 1, isolate
                                                                                                                                                                                                                                                                                                                      VRL 27-JUL-1995
                                                                                                                                                with
                                                                                                                                                                                   Muratori, L.,
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                                                                                                                                                                      Baralle, F.B.
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                  HPCEB11/c
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       DEFINITION
                                         RESULT 13
                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                       FEATURES
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AUTHORS
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HPCEB1/c
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ORIGIN
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                                                                               74
HPCEB11 149 bp Hepatitis C virus (HCV) genomic
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-DEC-1991) Shiu-Wan Chan, University of Edinburgh, Medical School, Dept. of Medical Microbiology; Teviot Place, Edinburgh EH8 9A6, U.K. (E-mail:ECH@CASTLE.ED.AC.UK, Tel:031-650-3138, Fax:031-662-4135)
                                                                                                                                                                                                                                                  Phone:
                                                                                                                                                                                                                                                                                             Edinburgh EH8 9AG
                                                                                                                                                                                                                                                                                                               Teviot Place
                                                                                                                                                                                                                                                                                                                             Medical School
                                                                                                                                                                                                                                                                                                                                         Department of Medical Microbiology University of Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Follett, E., Yap, P.L. and Simmonds, P. Analysis of a new hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus (isolate:E-b1) cDNA to genomic Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus (HCV) genomic D10114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relationship to existing variants
J. Gen. Virol. 73 (Pt 5), 1131-1141 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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CGGTGTACTCACCGGTTCCGCAGACCACTATGGC
                             CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bases 1 to 149)
                                                              Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,S.W., McOmish,F., Holmes,E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                               ECH@CASTLE.ED.AC.UK
                                                                                                                                                                                                                                     031-662-4135
                                                                                                                                       /db_xref="taxon:11103"
48 c 47 g
                                                                                                                                                                       /organism="Hepatitis C
/isolate="E-b1"
                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                 (25-Dec-1991) to DDBJ by:
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40 c
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                                                                          66.7%;
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Pred. No. 4.7e
0; Mismatches
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4.7e+02;
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                                                                                          DB 14;
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41
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                                                                                        Length 149;
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                                                          Indels
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RNA,

RNA linear VRL 02-FEB-1999
1, 5'non-coding region.

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JOURNAL
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REFERENCE
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ORGANISM
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HPCEB12/c
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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ORIGIN
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                                                          AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   74
Direct Submission
Direct Submission
Submitted (25-DEC-1991) Shiu-Wan Chan, University of Edinburgh,
Submitted (25-DEC-1991) Shiu-Wan Chan, University of Edinburgh,
Medical School, Dept. of Medical Microbiology; Teviot Place,
Medical School, Dept. of Medical Microbiology; Teviot Place,
                                                                                                                                                                                                                                                                                                                                                                                                                              D10118
D10118.1
                                                                                                                    Follett, E., Yap, P.L. and Simmonds, P. Analysis of a new hepatitis C virus type and relationship to existing variants J. Gen. Virol. 73 (Pt 5), 1131-1141 (1992)
                                                                                                                                                                                                                                                   Hepatitis C virus (isolate:E-b12) cDNA Hepatitis C virus
                                                                                                                                                                                                                                                                                                                   Heatitis C virus (HCV) D10119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Medical Microbiology University of Edinburgh Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-DEC-1991) Shiu-Wan Chan, University of Edinburgh, Medical School, Dept. of Medical Microbiology; Teviot Place, Edinburgh EHB 9AC, U.K. (E-mail:ECH@CASTLE.ED.AC.UK, Tel:031-650-3138, Fax:031-662-4135)
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J. Gen. Virol. 73 (Pt 5), 1131-1141 (1992)
                                                                                                                                                                                    Chan, S.W., McOmish, F.,
                                                                                                                                                                                                                                                                                                    D10119.1 GI:221551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E mail: ECH@CASTLE.ED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shiu-Wan Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-Dec-1991) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan, S.W., McOmish, F.,
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                                                                       Chan, S.-W.
                                                                                                                                                                                                                    Hepacivirus.
                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand.viruses,
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                                                                                      (bases 1 to 149)
                                                                                                                                                                                                 (bases 1 to 149)
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47 c 42 g
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/isolate="E-bl1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC.UK
                                                                                                                                                                                                                                                                                                                                  149 bp
genomic RNA,
                                                                                                                                                                                    Holmes; E.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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0;
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                                                                                                                                                                                                                                                                                                                               RNA linear VRL, 5'non-coding region.
                                                                                                                                                                                  Dow, B.,
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ORGANISM
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ORIGIN
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HPCEB13/c
BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                  Direct Submission
Submitted (25-DEC-1991) Shiu-Wan Chan, University of Edinburgh,
Medical School, Dept. of Medical Microbiology; Teviot Place,
Edinburgh EH8 9AG, U.K. (E-mail:ECH@CASTLE.ED.AC.UK,
Tel:031-650-3138, Fax:031-662-4135)
Submitted (25-Dec-1991) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus (HCV) genomic D10120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Follett, E., Yap, P.L. and Simmonds, P. Analysis of a new hepatitis C virus type a relationship to existing variants
J. Gen. Virol. 73 (Pt 5), 1131-1141 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus (isolate:E-bl3) cDNA Hepatitis C virus
                                                                                                                                  E mail: ECH@CASTLE.ED.AC.UK
                                                                                                                                                                                             University of Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chan, S.W., McOmish, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shiu-Wan Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel:031-650-3138, Fax:031-662-4135) Submitted (25-Dec-1991) to DDBJ by:
                                                                                                                                                              Edinburgh EH8
                                                                                                                                                                                                                         Department of
                                                                                                                                                                                                                                            Shiu-Wan Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stagė; Flaviviridae;
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                           /isolate="E-bl3"
/db_xref="taxon:11103"
                                                       /organism="Hepatitis C
                                                                       1. .149
                                                                                  Location/Qualifiers
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*	Search comp Job time :	Db .	Query Match Best Local Matches 3
•	Search completed: July 10, 2003, 19:20:01 Job time : 286.951 secs	1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC	Query Match  Best Local Similarity 97.1%  Matches 33; Conservative
	19:20:01	FTCCGCAGACCACTATGGC 33	Score 22; DB 14; Length 149; Pred. No. 4.7e+02; O; Mismatches O; Indels
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Run on:
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July 10, 2003, 18:15:27; Search time 242.625 Seconds (without alignments) 3358.597 Million cell updates/sec
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Scoring table: Title: Perfect score: Searched: Sequence: 2054640 seqs, 14551402878 residues IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0 US-10-087-631B-7 28 gcaagcaccctatcaggcagtaccacaa 28

Total number of hits satisfying chosen parameters:

4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:\* gb\_ba:\* gb\_htg:\* gb\_in:\* \_om:

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_hum:\*
em\_htgo\_mus:\*
em\_htgo\_other:\*

em\_htg\_vrt:\*

em\_htg\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20-JUN-2002

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Query Match
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                   1 Similarity
28; Conserv
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AX147022
                                                                                                                                                                                                         artificial sequences:
1 (bases 1 to 28)
Weindel, K., Riedling, M. and Geiger, A.
                                                                                                                                                                                                                                                                                AX147022.1
                                                                                                                                                                                                   fagnetic glass particles,
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28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified nucleic acid amplification Patent: US 6001611-A 4 14-DEC-1999;
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                                                                  /mod_base=OTHER
                                                                                                         /note="Synthetic oligonucleotide (HCV reverse)"
28
                                                                                note="derivatization with a p-(t-butyl)benzyl-residue"
                                                                                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
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               173305
                                                                                                                                                                                                                Detection and amplification or rna of dna by rna ligase Patent: WO 0179420-A 1 25-OCT-2001; MOLECULAR STAGING, INC. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                      synthetic construct. synthetic construct
                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                             artificial sequences.
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11 c 18 g 1:
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1 (bases 1 to 186)
Funahashi,S. and Hasegawa,A.
HCV ANTI-SENSE RNA, MANIFESTATION VECTOR CONTAINING THE SAME,
THERAPEUTIC AGENT FOR HCV-INVOLVED DISEASE CONTAINING THE RNA
                                                                                                                                        186 bp RNA linear sense RNA against partial sequence of 5'UTR of
                                                                                                                                                          E10302
                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                  Kessler,C., Bartl,K., Haberhausen,G. and Orum,H. Specific and sensitive method for detecting nucleic Patent: WO 9923250-A 47 14-MAY-1999; KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK) Location/Qualifiers
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Sequence 47 from Patent
AX021668
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Marshall,R.L., Carrino,J.J. and Sustachek,J.C.
Amplification of RNA sequences using the ligase chain reaction
Patent: US 5686272-A 36 11-NOV-1997;
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173305.1
                                                                   unidentified
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Hepatitis C virus
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Kessler,C., Bartl,K.,
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/db_xref="taxon:11103"
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9 c 23 g
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                                                                                                                                                                                                                                             Nucleic acid compounds and screening Patent: WO 0144266-A 5 21-JUN-2001;
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llarity 100.0%;
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L3-MAY-1994 JP 1994124609
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1. .187
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Location/Qualifiers
                                                                                                                                                              /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Probe"
48 c 64 g 40 t
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/db_xref="taxon:32644"
65 c 48 g 3
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Submitted (07-JAN-1998) Hepatitis Laboratory,
Submitted (07-JAN-1998) Aires, Paraguay 2155 11t
                                                                                                                                                                                                                       quarleri,J.F., Robertson,B.H., Mathet,V.L., retu, r., were requestio,M.P., Mando,O., Carballal,G. and Oubina,J.R. Genomic and phylogenetic analysis of hepatitis C virus isolates from argentine patients a six-year retrospective study J. Clin. Microbiol. 38 (12), 4560-4568 (2000)
                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
Hepatitis C virus
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Direct Submission

Direct Submission

Direct Submitted (07-JAN-1998) Hepatitis Laboratory, Faculty of Medicine,

Submitted (07-JAN-1998) Paraduav 2155 11th, Buenos Aires 1121,
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                                                                     'organism="Hepatitis C
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/isolate="611"
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                                                                                                                           Faculty of Medicine, h, Buenos Aires 1121,
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                                             Quarleri,J.F., Robertson,B.H., Mathet,V.L., Feld,M., Espinola,L. Requeijo,M.P., Mando,O., Carballal,G. and Oubina,J.R. Genomic and phylogenetic analysis of hepatitis C virus isolates
                                                                                                                                                                                             Hepatitis C virus isolate AF041277
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                    from argentine patients: a six-year retrospective study J. Clin. Microbiol. 38 (12), 4560-4568 (2000)
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Hepatitis C virus
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                                                                                                                        Viruses;
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Direct Submission
Submitted (07-JAN-1998) Hepatitis Laboratory, Faculty of Medicine,
Submitted (07-JAN-1998) Hepatitis Laboratory, Faculty of Medicine,
University of Buenos Aires, Paraguay 2155 11th, Buenos Aires 1121,
                                                                                                           Tepacivirus.
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Hepatitis C virus
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/isolate="760"
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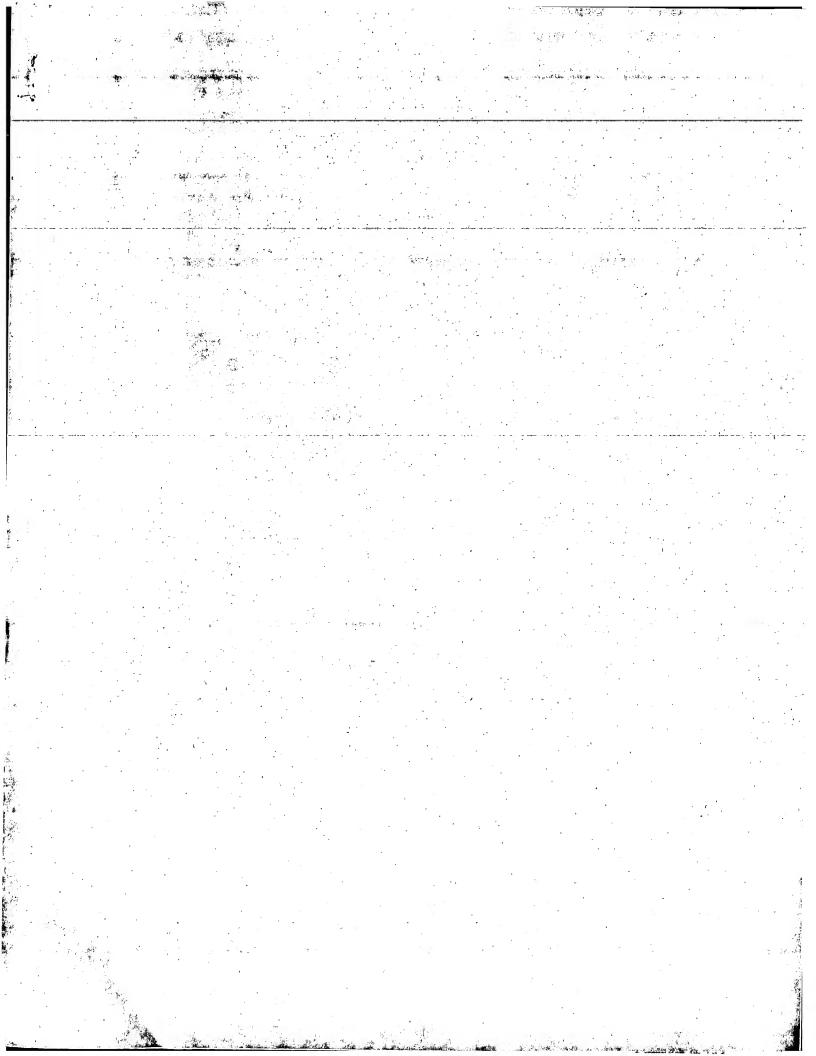
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           AF041289 191 bp ss-RNA linear V
Hepatitis C virus isolate 818 5' untranslated region.
AF041289
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Quarleri,J., Robertson,B.H. and Oubina,J.R.
Direct Submission
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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Hepatitis C virus isolate 784 5' untranslated region
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/isolate="784"
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/isolate="768"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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University of Buenos Aires, Paraguay 2155 11th,
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/isolate="818"
/db_xref="taxon:11103"
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	RESULT 1 AR054575 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		4 4 4 2 2 2 2 2 3 4 4 3 2 2 2 3 3 3 3 3	37 38 39	3 3 3 5 5	333 330	30 30	27	2 C C C	220	17 18	15 15	11 12	c 10	8	ത ഗ്ര	ا س حـ	N ← .	Result No. S
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                                                                                                                       /mod_base=OTHER
                                                                                                                                                                                          /note="Synthetic oligonucleotide primer (HCV forward)"
                                                                                                                                                /note="derivatization with a p-(t-butyl)benzyl-residue"
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                                                                                                                                                  KESSLER CHRISTOPH (DE); BARTL KNUT (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK LOCATION/Qualifiers
                                                                                                                                                                                     Kessler,C., Bartl,K., Haberhausen,G. and Orum,H. Specific and sensitive nucleic acid detection method Patent: WO 9924606-A 50 20-MAY-1999;
                                                                                                                                                                                                                                         Hepatitis C virus.
Hepatitis C virus
Viruses; sRNNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                              Sequence 50 from Patent WO9924606.
                                                           Similarity
                                                                                                                                                                                                                 1 (bases 1 to 51)
Kessler,C., Bartl,K.,
                     GCAGAAAGCGTCTAGCCATGGCGTTA 26
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26; Conserv
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Self-replicating rna molecule from hepatitis
Patent: WO 02052015-A 17 04-JUL-2002;
BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus.
Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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Sequence 17 from Patent W002052015.
GCAGAAAGCGTCTAGCCATGGCGTTA
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ilarity 100.0%;
Conservative (
                                                                                                         /organism="Hepatitis C virus"
/db_xref="taxon:11103"
12 c 15 g 13 t
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/db_xref="taxon:11103"
7 c 9 g 6 t
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                                                      Score 26; DB 6;
Pred. No. 0.057;
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Pred. No. 0.0
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RESULT 8
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HPCUT6CLN
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           Hepatitis C vi
M94467 M84479
M94467.1 GI:3
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Esteban,R., Guardia,J. and Gomez,J.
Hepatitis C virus (HCV) circulates as a
                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus RNA. Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                         M94468 M84479
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                                                                                                                                                                                                                                                                                                                                                     Viruses;
                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein.
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 nonstructural protein
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                                                                                            GCAGAAAGCGTCTAGCCATGGCGTTA 48
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/db_xref="taxon:11103"
35 c 36 g 24 t .
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/db_xref="taxon:32630"
/note="Probe"
20 c 23 g 18 t
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                             vrL 02-AUG-1993
gene, 5' flank.
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{5' region} [hepatitis
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                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 152236] from the original journal article. This sequence comes from Fig. 1.

Location/Qualifiers
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Hepatitis C virus
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/db_xref="taxon:11103"
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from patent US 6001990.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                             1 (bases 1 to 160)
Martell,M., Esteban,J.I.,
Esteban,R., Guardia,J. an
Hepatitis C virus (HCV) c
                                                                                           Hepatitis C virus RNA.
                                                                         Viruses; ssRNA positive-strand viruses, no
                                                                                                                           M94466.1 GI:329982
                                                                                                               nonstructural protein.
                                                                                                                                                          HPCUT74CLN
                                                                                                                                                  Hepatitis C
                                                                        epacivirus.
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 156)
Cha, T.-A., Kolberg, J., Irvine, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus cDNA to genomic RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus isolate M74253
                    osely related genomes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (Dases 1 to 155)

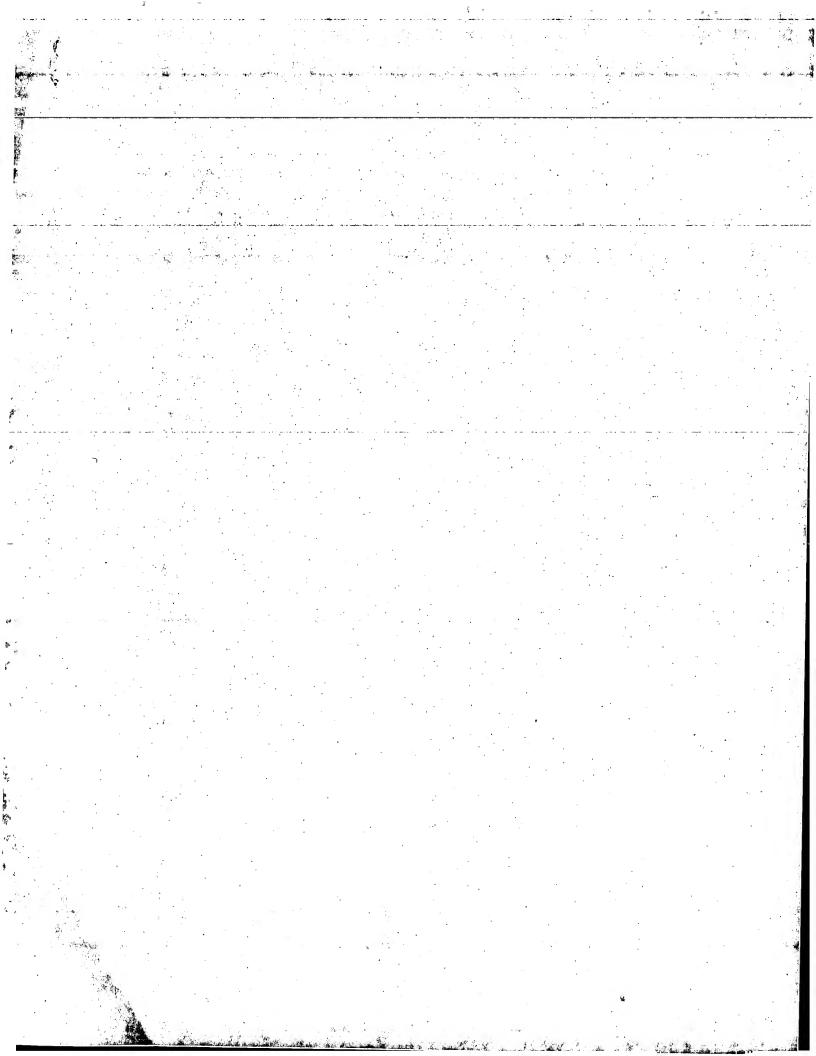
Hands, J.R., Wakita, T. and Moradpour, I Antisense inhibition of hepatitis C. Patent: US 6001990-A 41 14-DEC-1999,
                                                                                                                                                                                                        GCAGAAAGCGTCTAGCCATGGCGTTA 35
                                                                                                                                                                                                                      GCAGAAAGCGTCTAGCCATGGCGTTA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified
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                                                                                                                                                                                                                                                                                            31 a
position
                                                                                                                                                                                                                                                                                                                                                               detection of viral RNA in
                                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                           .0.-L., Houghton, M., Kuo,
                                                                                                                                     M84479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                    /organism="Hepatitis C virus"
/db_xref="taxon:11103"
48 c 45 g 32 t
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:329742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
43 c 51 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .155
                                                                                                                                             virus (clone
                                                                                                                                                                                                                                                   0;
                                        and Gomez, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                 circulates as quasispecies
                                                                                                                                                                                                                                                           Score 26; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB
Pred. No. 0.0
); M1smatches
                                                                                                                                         160 bp ss-RNA
#74) nonstructural
                                               Quer,J.,
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Kuo, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 bp ss-RNA
I1 genome, 5'
                                                                                                                                                                                                                                                                                                                                                               sequence of human serum
                                                                                                                                                                                                                                                                                                   32 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 t
                                                                                                                                                                                                                                                                    DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                             Genesca,J.,
                                                                                                                                                                                                                                                                                                                                                                                            Stempien,
                                                                                                                                                                                                                                                      .054;
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                nature
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                       population of different
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                                                                           DNA stage;
                                                                                                                                                                                                                                                                  Length 156;
                                                                                                                                                                                                                                                                                                                                                              and plasma
                                                                                                                                                                                                                                                                                                                                                                                 and Urdea;M
                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 155;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA stage; Flaviviridae;
                                                                                                                                          protein
              of HCV genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                           Weiner, A.,
                                                                                                                                                                                                                                                                                                                                                                                Beall, E., Yano, M., Irdea, M.S.
                                                                                                                                         gene,
                                                                                                                                                     VRL.
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRL 02-AUG-1993
                                                                          Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                         02-AUG-1993
e, 5' flank.
                                                                                                                                                                                                                                                                                                                                                                      C virus for
                                                                                                                                                                                                                                             Gaps
                                                                                                                          DEFINITION
ACCESSION
VERSION
                                                                                                                                                          RESULT 14
HPCUT34CLN
LOCUS
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ORGANISM
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HPCUT56CLN
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Matches 26
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Query Match
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                                                                                                            Hepatitis C 1
M94461 M84471
M94461.1 GI
                                                                                                                                                                                            1 (bases 1 to 176)
Martell,M., Esteban,J.I.,
Esteban,R., Guardia,J. and
Hepatitis C virus (HCV) ci
                                                             Viruses; ssRNA positive-strand viruses,
                                                                             Hepatitis C virus RNA. Hepatitis C virus
                                                                                                  nonstructural
                                                        depacivirus.
                                                                                                                                            HPCUT34CLN
                                                                                                                                                                                                                                                                                                                                                                 distribution J. Virol. 66
                                                                                                                                                                                                                                                                                                                                                                                 Esteban, R., Guardia, J. and Gomez, J. Hepatitis C virus (HCV) circulates as closely related genomes: quasispecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nonstructural protein.
Hepatitis C virus RNA.
Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 171)
Martell, M., Esteban, J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M94464.1
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepacivirus.
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92219420
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                                                                                                             GI:329976
                                                                                                                                                                                                                                                                                     /organism="Hepatitis C virus"
/db_xref="taxon:11103"
51 c 47 g 36 t
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:329980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hepatitis C virus"
/db_xref="taxon:11103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .160
                                                                                                                                 virus (clone
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                                                                                                 protein
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Pred. No. 0.0
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Pred. No. 0.0
0; Mismatches
            circulates
 quasispecies
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                                Quer, J.,
                      Gomez, J
                                                                                                                                                                                                                                                                                                                                                                                                         Quer,J.,
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#56)
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                                                                                                                             nonstructural
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) nonstructural
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                            Genesca, J.,
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                                                                                                                                                                                                                                               .053;
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population of ature of HCV gr
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                                                               no
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                                                            DNA stage;
                                                                                                                            linear
l protein
                                                                                                                                                                                                                                                      Length 171;
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                             Weiner, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              stage;
                                                                                                                          VRL 02-AUG-1993 gene, 5' flank.
         different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRL 02-AUG-1993 gene, 5' flank.
                                                            Flaviviridae;
                                                                                                                                                                                                                                  0;
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(5),

3225-3229 (1992)

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BASE COUNT
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Search completed: July 10, 2003, 19:20:22
Job time: 227.294 secs
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HPCUT38CLN
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonstructural protein.
Hepatitis C virus RNA.
Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus (clone #38) nonstructural protein gene, 5' flank. M94462 M84479
                                                                                                                                                                                                                                                                                             1313927
                                                                                                                                                                                                                                                                                                                                                        Martell,M., Esteban,J.I., Quer,J., Genesca,J., Welner,A.,
Esteban,R., Guardia,J. and Gomez,J.
Hepatitis C virus (HCV) circulates as a population of different but
closely related genomes: quasispecies nature of HCV genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M94462.1 .GI:329977
                                                                                                                                                                                                                                                                                                               istribution
. virol. 66 (5), 3225-3229 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 176)
                                                                                                                          100.0%; Score 26; DB 14; Length 176; ilarity 100.0%; Pred. No. 0.053; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 26; DB 14; Length 176; ilarity 100.0%; Pred. No. 0.053; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                       /organism="Hepatitis C virus"
/db_xref="taxon:11103"
51 c 51 g 38 t
                                                                                                                                                                                                                                                             Location/Qualifiers
1. .176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hepatitis C virus"
/db_xref="taxon:11103"
50 c 51 g 38 t
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1. .176
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PCT-US95-13552-14
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685.785 Million cell updates/sec
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US-08-470-426B-15
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US-09-677-218B-21	US-08-851-588-21	US-08-934-097A-21	US-09-034-205-21	US-08-520-946-129	US-08-520-946-128	US-08-520-946-123	US-08-757-653-129	US-08-757-653-128	US-08-757-653-123	US-09-677-192-27	US-09-677-192-26	US-09-677-218B-27	US-09-677-218B-26	US-08-851-588-27	US-08-851-588-26	US-08-934-097A-27	US-08-934-097A-26
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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Apr	App	App	App					, App									App

## ALIGNMENTS

15, Appli 5. 5856458

Application US/08470426B

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; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-470-426B-15
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 241; Conservative 0;
                                                                                                                                                                            TELEFAX: (202) 659-14 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                         NAME: Weilacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
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                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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ADDRESSEE: L.L.P:
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DEDNESS: single
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Nakamura, Tetsuo
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SYSTEM: PC-DOS/MS-DOS
                                                                                               unknown
                                                                                                                                                                                                             (202)
                                                                              DNA (genomic)
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Score 241; DB 2;
Pred. No. 1.5e-68;
; Mismatches 0;
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 1APO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                LENGTH: 341 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wakita, Takaji | TITLE OF INVENTION: CHIMERIC HEPATITIS B/HEPATITIS C VIRUS VACCINE
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
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                                           68 GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
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CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC 120
                                                                     19103
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                                                                                                               Conservative
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                                                                                                       Score 241; DB 3;
Pred. No. 1.6e-68;
; Mismatches 0;
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; ORGANISM: Hepatitis C virus
US-09-014-416-47
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US-09-014-416-47
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LENGTH: 341
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CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: US 60/053,062
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Emerson, APPLICANT: Purcell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: Purcell, Robert H."
ITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES
ITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                             Local Similarity
                                             308 C 308
                              241 C 241
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                                                                                                                121 GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCGGGAGAC
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.6e-68;
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RESULT 4
US-09-014-416-48
Sequence 48, Application US/09014416; Patent No. 6153421

GENERAL INFORMATION:

APPLICANT: Bukh, Jens
APPLICANT: Emerson, Susanne
APPLICANT: Purcal'

Emerson, Susanne U. Purcell, Robert H.

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; ORGANISM: Hepatitis C virus
US-09-014-416-48
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Best Local Similarity 100.
Matches 241; Conservative
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SEQ ID NO 48
LENGTH: 341
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EARLIER APPLICATION NUMBER: US 60/053,062
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                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                        ADDRESSEE: WOULD ADDRESSEE: No. 6235888ris
ADDRESSEE: No. 6235888ris
ADDRESSEE: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF
TORNEY/AGENT INFORMATION:
                                                                                            FILING DATE:
                                   APPLICATION NUMBER:
                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                         USA
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Zurawski, Jr., Vincent R.
Coney, Leslie R.
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                                                                                                                                                                                                                                                                                                                                              Woodcock, Washburn, Kurtz, Mackiewicz
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                                  US/08/318,248
                                                                                                           US/08/869,380
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Pred. No. 1.6e-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine
                                                                                                                                               #1.25
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: AP
TELECOMMUNICATION INFORMATION:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,248
FILING DATE: 05-OCT-1994
                                                                                                                          SOFTWARE: WordPerfect .5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     ITLE OF INVENTION:
                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                       CLASSIFICATION
                                                                                          FILING DATE:
                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodco
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                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                            STREET:
 CLASSIFICATION
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19103
'R RF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Zurawski, Jr., Vincent R. Coney, Leslie R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wands, Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pachuk, Catherine J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tokushige, Katsutoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linear
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                                                                                                                                                                                                                                                                                                                                              Woodcock, Washburn, Kurtz, Mackiewicz
                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                        Liberty Place, 46th floor
                                                                                          Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
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568-3439
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                                                                                                           PCT/US95/13552
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Pred. No. 1.6e-68;
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-08-474-700B-39/c
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            FILING DATE: 07-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                 COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 341 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wakita, Takaji
APPLICANT: Moradpour, Dar
FILING DATE:
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
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REFERENCE/DOCKET NUMBER: APOL-0238
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                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                            02110-2804
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                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                            INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
SEQUENCES: 45
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                                                                                                                                                                                                                           Massachusetts '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08474700B
                                                                                                                                                                                                                                                            225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                       Wands, Jack
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                                                                                                                                                                                                                                                                               Fish & Richardson
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                                                 07-JUN-1995
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                                                                US/08/474,700B
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US-08-988-321B-37
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FILING DATE: May 17, 1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
FILING DATE: MAY 30, 1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,093
FILING DATE: May 17, 1996
                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID .NO:
                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                ORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                               CLASSIFICATION:
                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                    OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.1 FOR WINDOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                ADDRESSEE: Law OILLCU
STREET: 66 East Main Street
                                                                                                                                                                                                                                                                                                                                                                               TILE OF INVENTION: Compositions An
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                                                                                                                                                                                                                                                                                  ITY: Marlton
TATE: NJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGTGTACTGCCTGATAGGGTGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-8906
                                                                                                                                                                                                                                                                                                                       Law Offices of Jane Massey Licata
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                  08/452,841
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                                                                                                                                        US/08/988,321B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                Sequence 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 191;
                                                                                                                                                                                                                                                                                                                                               tent No. 6284458
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (856) 810-1454 (NFORMATION FOR SEQ ID NO: )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: March 9 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: September 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,257 REFERENCE/DOCKET NUMBER: IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEPHONE:
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata,
STREET: 210 Lake Drive East, S
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGUCCUUUCUUGGAUCAACCCGCTCAAUGCCUGGAGAUUUUGGGCGUGCCCCCGCGAGAC
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                           APPLICATION NUMBER: US/08/397,220B FILING DATE: 09-Mar-1995 CLASSIFICATION: <Unknown>
                                                                                                                                                                        COUNTRY: USA
ZIP: 08002
                                                                                                                                                                                                                    CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                Application US/08397220B
                                                                                                                                                                                                     STATE: NJ
                                                                                           SOFTWARE: WORDPERFECT 5,1
APPLICATION NUMBER: PCT/JP93/01293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/397,220
9, 1995
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                                                                                                                                                                                                                                                                                                   Hepatitis
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C Virus-Associated Diseases
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RESULT 10
US-08-650-093C-25
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                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08650093C Patent No. 6391542
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,093C
FILING DATE: 17-May-1996
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: ISPH-0031 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 UGCUAGCCGAGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUG
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                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.1 for Windows
                                                                                                                                                ZIP: 08053
                                                                                                                                                                                      STATE: NJ
                                                                                                                                                                                                        CITY: Marlton
                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jane Massey Licata REGISTRATION NUMBER: 32,257
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APPLICATION NUMBER: 07/945,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-Sep+93
APPLICATION NUMBER: JP 5-87195
FILING DATE: 14-Apr-93
                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
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                                                                                                                                                                       USA
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IO: 25:
                                                                                                                                                                                                                                                                                                                                       Anderson et al.
                                                                                                                                                                                                                                                                                                  Compositions And Methods For Treatment Hepatitis C Virus-Associated Diseases
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                                                                                                                                                                                                                                          & TYRRELL P.C
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Pred. No. 1.9e-68;
0; Mismatches (
                                                                                                               3.5 INCH,
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                                                                                                               1.44 Mb
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US-08-650-093C-25
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Best Local
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                                                                                                                                                                                                                                                                                                                 NERAL INFORMATION:
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        APPLICA
                      COMPUTER: IBM PS/2 Model 502 or 55SX OPERATING SYSTEM: MS-DOS (Version 5.) SOFTWARE: WordPerfect (Version 5.1)
                                                                                   MEDIUM
                                                                                                                              COUNTRY:
                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 1779-2400
                                                                                                                                                                     NDENCE ADDRESS:
SEE: Fish & Richardson
P: 225 Franklin Street
                                                                                                               02110-2804
                                                                             TYPE: 3.5" Diskette;
                                                                                                                                                               Boston
                                                                                                                                                                                                                                         INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                          .C 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: September 10, 1992 ORNEY/AGENT INFORMATION:
                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UGCUAGCCGAGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                        SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGUCCUUUCUUGGAUCAACCCGCTCAAUGCCUGGAGAUUUUGGGCGUGCCCCCGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTCCTTTCTTGGATCÅACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGGGAGAC
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                                                                                                                                                                                                                                                                                                                                   Application US/08474700B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: MAY 30, 1995
APPLICATION NUMBER: 08/397, 220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945, 289
                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/452,841
                                                                                                                                                                                                                                                                     Moradpour, Darius
                                                                                                                                                                                                                                                                                  Wakita, Takaji
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                                                                                                                                                                                                                                                                                                 Jack
                                                                                                                                                                                                                                     VIRUS
                                                                                                                                                                                                                                            ANTISENSE INHIBITION OF HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 241; DB 4; 79.3%; Pred. No. 1.9e-68;
US/08/474,700B
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Best Local
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  TITLE OF INVENTION: Hepatitis C Virus Vaccine NUMBER OF SEQUENCE: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICATION NUMBER:
                                                                                                                                                                                    ADDRESSEE: Woodcock, Washburn, Kurtz, ADDRESSEE: No. 6235888ris
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                                                                                                              19103
                                                                                                                                                       Philadelphia
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                                                                                                                                      PA
                                                                                                                                                                One Liberty Place, 46th floor
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307 240 247 120

127 60

187

USA

US/08/869, 380

Version #1.25

Zurawski, Jr., Vincent R. Coney, Leslie R.

Mackiewicz &

Takaji Catherine J.

Pachuk, Wakita,

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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 34,819
TELECOMMUNICATION INFORMATION: (617) 542-5070
TELEPAY: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 780 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER
                                                                   181 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
308 C 308
                           241 C 241
                                                248 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                                                                                                                              241;
                                                                                                                                                                                                             61 CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCCAGGACGACC
                                                                                                                                                                                                                                              68 GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
                                                                                                                                                                                                                                                                                                                                 h 100.0%;
Similarity 100.0%;
                                                                                                                                  GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGGGAGAC
                                                                                                                                                                                                                                                                 GAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCT
                                                                                                                 GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                              Score 241; DB 3
Pred. No. 2e-68;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                               DB 3;
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                                                                                                                                                                                                                                                                                                                                              Length 780;
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Query Match
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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   VE INVENTION: HEPATITIS VIRUS VACCINES VUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                          NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 568-3100
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
                                                                                      COUNTRY: UP
                                                                                                                                      ADDRESSEE: Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                               RRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                      Application PC/TUS9513552
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                                                                                                                                                                                                                                                             Zurawski, Jr., V
Coney, Leslie R.
                                                                                                                                                                                                                                                                                                                    Tokushige, Katsutoshi
Wakita, Takaji
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                                                                                                                                                                                                                                                                                                    Pachuk, Catherine J.
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                                                                                                                                                                                         Woodcock, Washburn, Kurtz, Mackiewicz &
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                                                                                                                                                                                                                                                                                                                                                       Jack
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                                                                                                                                                                                                                                                                                 Vincent R.
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Pred. No. 2.1e-68;
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RESULT 14
US-08-324-977-3
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Best Local Similarity
Matches 241; Conserv
                                                                                                                                                                                                                                                                    Sequence 3
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 568-34
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PC
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PRIOR APPLICATION NUMBER: US 08/318,248
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                                                            ORRESPONDENCE ADDRESS
                                                                              UMBER OF SEQUENCES:
                                                                                      PPLICANT: YOSHIDA, Iwao
"ITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE
"TILE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/467,859 FILING DATE: 06-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                              308 C 308
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                                                                                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                                                                                                                                     Application US/08324977
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                                                                                                                                                              MORI,:Chisato
TAKAMIZAWA, Akahisa
                                                                                                                                                                                                                             OKAYAMA, Hiroto
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                                  Armstrong, Westerman, Hattori, McLeland &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 241; DB 5; 100.0%; Pred. No. 2.1e-68;
N.W. Suite 1000
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241 C 241

239 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCCTTGTGGTACTGCCTGATAGGGTGCTTG 298

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Best Local
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ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.4***
CAMBUTER: IBM PC compatible
CAMBUTER: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1..1499
OTHER INFORMATION: /notOTHER INFORMATION: ID N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: | 2-230921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-AUG-1990 RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stevens-Smith, Theres REGISTRATION NUMBER: 36,281 REFERENCE/DOCKET NUMBER: 90 LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 31-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 2 FILING DATE: 25-JUN-1990
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                                                                                           119 CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                       GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
                                                                                                                                                                                                                      Similarity
            TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
                                                                GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
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RY: U.S.A.
GENT INFORMATION:
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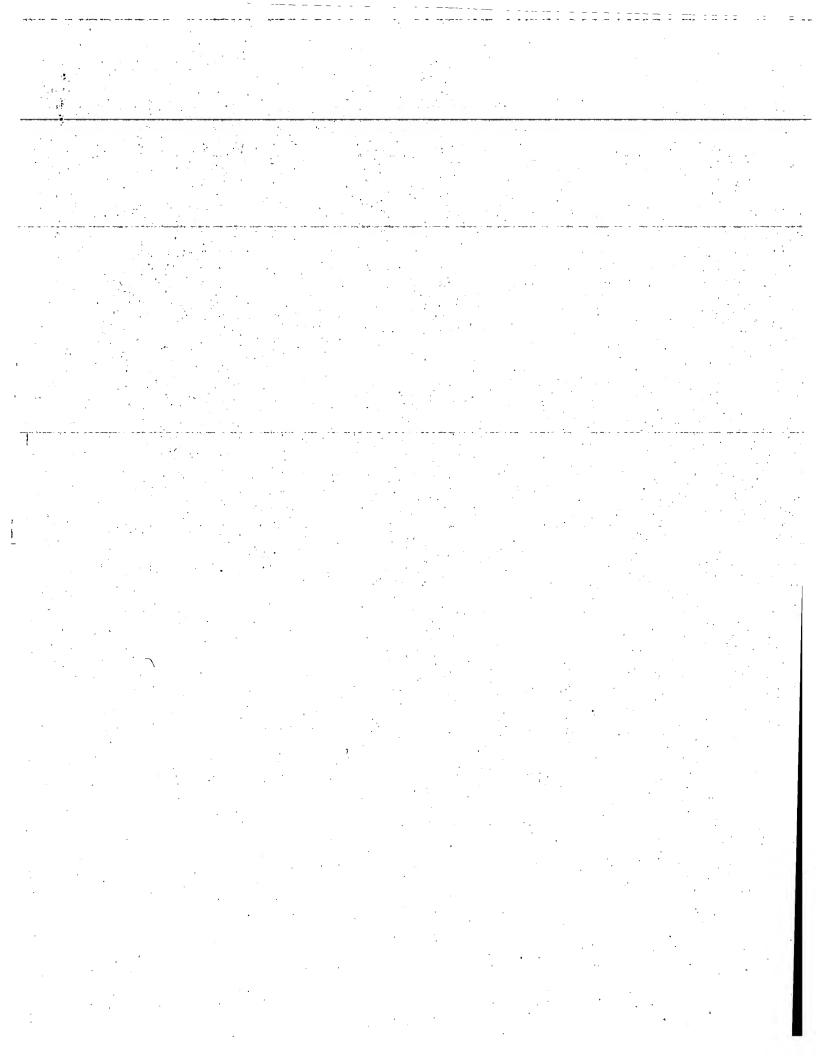
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RESULT 15
US-08-384-616-3
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NFORMATION FOR SEQ'ID NO:
SEQUENCE CHARACTERISTICS:
                                                      FEATURE:
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                                                                                                   FEATURE:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
10 2-230921
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/384,616
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                                                                   LOCATION:
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPTIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
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    Application US/08384616
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nucleic acid
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                    misc_feature
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TAKAMIZAWA, Akahisa
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      /note=
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Search completed: July 10, 2003, 20:28:04 Job time: 109.773 secs
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                                              299 C 299
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                                                                                        119 CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC 178
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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AV398524 AV398524
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AV398957 AV398957
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AU169952 AU16995	BG503487 602550	в 1020967 в 10209	вJ013902 вJ0139	AU169949 AU16994	вJ007208 ВJ007:	вJ487077 вJ4870	AU178284 AU17828	вJ011227 вJ0112	вл008203 вл0082	AU171278 AU17127	AU148437 AU14843	AA953786 oo38a04	BB165683 BB1656	BG254464 602369	BF218319 601881	BG333148 602430	AZ244546 RPCI-1	AK018050 Mus mu	BE260962 60115	C78921 C78921 N	AQ599676 HS_539	AL834604 AL83460	во552508 н40160	AL835471 AL83547	AV300075 AV3000	BG025626 602274	AW195/26 X085CU3.X	AK005732 Mus mu	8	8164 AV39	743 AV40	3450 AV39	53 AV39	V398803 AV39	V399052 AV39	8498 AV39	322 AV39

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## ALIGNMENTS

FEATURES Source		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AV398524 LOCUS DEFINITION
Project='Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a> , for whole ESTdb. Location/Qualifiers 1. 370	Genome Research Group.  National Institute of Radiological Sciences  National Institute of Radiological Sciences  Anagawa 4-9-1, Inage, Chiba 263-8555, Japan  Email: kmita@nirs.go.jp  method:uni-directional, sequence direction:sequenced from T3 primer	Dollay Colded; Dollay R. (Dases 1 to 370)  1 (Dases 1 to 370)  Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S. Bombyx mori cDNA Unpublished (2000)  Contact: Mita K	AV398524 AV398524.1 GI:6902176 EST. domestic silkworm. Bombyx mori Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Eukaryota; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombyx bombyx dasa Rombyx	AV398524 370 bp mRNA linear EST 05-FEB-2000 AV398524 Bombyx mori ovary BmNPV infected; 2 hr after inoculation Bombyx mori cDNA clone NV021911X T3, mRNA sequence.

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VERSION
KEYWORDS
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AW495169
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Mus musculus
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UT-M-BH3-aur-h-07-0-UI.sl NIH_BMAP_M_S4 Mus
UT-M-BH3-aur-h-07-0-UI 3', mRNA sequence.
AM495169
                                                                   AW495169.1 GI:7065415
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25; Conserv
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AU004535 Bombyx mori p50(Daizo)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mail: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jnpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #1ta,K., Morimyo,M.; Shimada,T., Okano,K. and Maeda,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
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Bombycoidea; Bombycidae; Bombyx.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 75.0
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGGAACTCTCCGTTCCGTGGCCCACTATCGC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nome Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGTACTCACCGTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       act: Mita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bases
                                                                                                                                                                                                                                                                                                                                            82 a
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                       /organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws20577"
                                                                                                                                                                                                                                                                                                                                    /clone_lib="Bombyx mori p50(Daizo)"
125 c 147 g 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'CREST project by JST'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tisue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr after inoculation"
/dev_stage="BmNPV infected; 2 hr after inoculation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 to 466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Bombyx mori ovary BmNPV infected; 2 hr after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:70
/clone="NV021911x"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Bombyx mori"
                                                                                                                                                                                                                                                                           61.2%;
75.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.2%;
75.8%;
                                                                                                                                                                                                                                                               Score 20.2; DB 9;
Pred. No. 5.7e+02;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20.2; DB 10
Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bombyx mori cDNA clone ws20577,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                          Length 466;
                                                                                                                          linear
                                                                                                                                                                                                                                                               Indels
                                                                                                           musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                       EST 24-FEB-2000
                                                                                                         cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 19-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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밁 Ş

165 CAGTGTATCCAGAGCTCCGCAGTCAACTATGGC 197 1 CGGTGTACTCACCGTTCCGCAGACCACTATGGC Query Match Best Local Similarity

61.2%; 75.8%;

Matches

Conservative

0,

Score 20.2; DB 10; Pred. No. 6.1e+02; 0; Mismatches 8;

Indels Length

0;

Gaps

0

616;

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ORIGIN
                           BASE COUNT
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENERICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               considered under appropriate and limited collaborative arrangements Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 301.443 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 616)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Chin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20892-9643
                           137
                                                                                                                                                                                       NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S3.1,
NIH_BMAP_M_S3.1 The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCRamplified
cDNA inserts from NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.1 NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (LifeTechnologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
                    TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=basal-ganglia
TAG_SEQ=TGTAC"
179 c 148 g 152
                                                                                                                                                  described (Bonaldo, Lennon 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been representation of cDNAs from which ESTs had already been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH108 (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
/corehallum brain tens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cortex, amygdala, basal ganglia, pineal gland hipoccampus) after a series of subtractions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerebellum, brain stems, olfactory bulbs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="UI-M-BH3-aur-h-07-0-UI"
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                148 g
                152 t
                                                                                                                                                                      Soares, Genome Research
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REFERENCE
AUTHORS
TITLE
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AV399654
LOCUS
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VERSION
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ORGANISM
                                                                                                 COMMENT
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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VERSION
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AV398282
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                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                           AV399654 Bombyx mori ovary BmNPV infected; 12 hr after inoculation Bombyx mori cDNA clone NV120518 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                         Mita,K., Morimyo,M.,
Bombyx mori cDNA
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV398282 Bombyx mori ovary BmNPV infected; 2 hr after Bombyx mori cDNA clone NV021341 T3, mRNA sequence.
method:uni-directional, sequence direction:sequenced (5' \rightarrow 3')
                            Anagawa 4-9-1, Inage, Cl
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                               Bombyx mori
                                                                                                                                                                                                                                                                                AV399654.1. GI:6903306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Future Program in JSPS'. see 'SilkBase', for whole ESTdb. <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for whole ESTdb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method:uni-directional, sequence direction:sequenced from T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anagawa 4-9-1, Inage, Ch
Email: kmita@nirs.go.jp
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                              Genome Research Group
National Institute of
                                                                                               Contact: Mita
                                                                                                                                                         Neoptera; Endopterygota; Lepidop
Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 667)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mita,K., Morimyo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV398282.1
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                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of
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Bombycoldea; Bombycidae; Bombyx.
1 (bases 1 to 650)
                                                                                                                                                                                                                                              domestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project='Silkworm Genome Program in MAFF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iomestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGGAACTCTCCGTTCCGTGGCCCACTATCGC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGTGTACTCACCGTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr
182 c 199 g 153 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV021341"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inoculation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="Bombyx mori ovary BmNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:6901934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
75.8%;
                                                                                                                                             Shimada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20.2; [Pred. No. 6.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimada, T., Okano, K.
                                            Chiba
                                             Radiological Sciences
Chiba 263-8555, Japan
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Chiba 263-8555, Japan
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                                                                                                                                                                                            Lepidoptera;
                                                                                                                                                                                                             Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hexapoda; Insecta; Pterygota;
ptera; Glossata; Ditrysia;
                                                                                                                                             Okano, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2e+02;
8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                           oda; Insecta; Pterygota;
Glossata; Ditrysia;
                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          after inoculation 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Maeda, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                             Maeda,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research
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               13
               primer
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                                                                                                                                BASE COUNT
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AV398957
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79
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AV398957 Bombyx mori ovary EmNPV infected; 6 hr after ESBONDYX mori cDNA clone NV060470 T3, mRNA sequence.
AV398957
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                                                                                                                                                                                                                                                                                              Project-'Silkworm Genome Program in MAFF, and Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for
                                                                                                                                                                                                                                                                                                                                                                         Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
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                                                                                                                                                                                                                                                                                                                                             method:uni-directional, (5' -> 3')
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota;
Bombycoidea; Bombycidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domestic silkworm.
                                                                     Similarity
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                          CGGTGTACTCACCGTTCCGCAGACCACTATGGC 33
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                                                                                                                            /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 6
186 c 202 g 154 t
                                                                                                                                                                                                                     /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV060470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="BMN cultured cell"
/dev_stage="BMNPV infected; 12
188 c 198 g 153 t
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/clone="NV120518"
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Endopterygota; Lepidoptera; Glossata; Ditrysia;
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                                                       Score 20.2; In Pred. No. 6.3e 0; Mismatches
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                                                    e 20.2; Db iv,
No. 6.3e+02;
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No. 6.
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method:uni-directional, sequence direction:sequenced from
                                                                                                                                                                                                                                                                       AV398498 Bombyx mor! ovary BmNPV infected; Bombyx mor! cDNA clone NV021881 T3, mRNA s
                    Anagawa 4-9-1, Inage, Cl
Email: kmita@nirs.go.jp
                                                National Institute of
                                                                 Genome Research Group
                                                                                               Unpublished (200
                                                                                                                                                                                                                                                                 AV398498
                                                                               Contact: Mita K
                                                                                                                         Mita, K., Morimyo, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project='Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS'. see 'SilkBase', 'Anttp://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb. Location/Qualifiers
                                                                                                                                                   ombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                      ukaryota;
                                                                                                                                                                                                                omestic silkworm.
                                                                                                                                                                 eoptera; Endopterygota;
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Unpublished (2000)
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Neoptera; Endopterygota; Lepidoptera; Glossata;
Bombycoldea; Bombycidae; Bombyx.
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National Institute of Radiological Sciences
National -9-1, Inage, Chiba 263-8555, Japan
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                                                                                                                                       (bases 1 to 677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr
190 c 206 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Bombyx mori ovary BmNPV infected;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="NV021679"
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/db_xref="taxon:7091"
                                                                                                                                                                                      Metazoa;
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                                                                                             (2000)
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                                                                                                                                                                            Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                            GTGGCCCACTATCGC 114
                                                                                                                   Shimada, T., Okano, K. and Maeda, S
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                                              Radiological Sciences
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                                Chiba 263-8555,
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82 CGCGGAACTCTCCGTTCCGTGGCCCACTATCGC
                                1 CGGTGTACTCACCGTTCCGCAGACCACTATGGC
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AV399052 Bombyx mori ovary BmNPV infected;
Bombyx mori cDNA clone NV060603 T3, mRNA st
AV399052
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                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kmita@nirs.go.
                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bombyx mori cDNA
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mita
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1 (bases 1 to 677)
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Neoptera; Endopterygota; Lepidoptera; Glossata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                    Project='Silkworm Genome Program in MAFF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGTGTACTCACCGTTCCGCAGACCACTATGGC 33
                                                                                                                                                         121
                                                                     Conservative
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llarity 75.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  uni-directional, sequence direction: sequenced from 13 primer
                                                                                                                                                  /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 6 l
/dev_stage="205 g 157 t
                                                                                                                                                                                                                                  /clone_lib="Bombyx mori ovary BmNPV
                                                                                                                                                                                                                                                           /clone="NV060603"
                                                                                                                                                                                                                                                                         /organism="Bombyx mori"
/db_xref="taxon:7091"
                                                                                                                                                                                                                         inoculation"
                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr after inoculation"
191 c 203 g 158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Bombyx mori ovary BmNPV infected; 2 hr after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bombyx mori"
/db_xref="taxon:7091"
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                                                                                   61.2%;
75.8%;
                                                                                 Score 20:2;
Pred. No. 6.
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Pred. No. 6.3e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bombyx
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                                                                                   .3e+02
                                                                                                   DB
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                                                                                                   10;
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ssata; Ditrysia;
                                                                 Indels
                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                       and Research for the
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                                                                                                                                                                                                                                    infected;
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BASE COUNT
ORIGIN
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AV398253
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AUTHORS
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ORGANISM
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AV398803
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                                                                                                                                  REFERENCE
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ORGANISM
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Best Local S
Matches 25
                                                                                                     AUTHORS
TITLE
                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                              Mita,K., Morimyo,M., Si
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
                                                                                                                                                                                                                                                                                                                                                                                              82 CGCGGAACTCTCCGTTCCGTGGCCCACTATCGC 114
                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Neoptera; Endopterygota; Lepidoptera; Glos Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                              AV398253 Bombyx mori ovary EmNPV infected; 2 hr after inoculation
                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGGTGTACTCACCGTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, Location/Qualifiers
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National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
                                                                                                                                                                                                                                                  AV398253.1 GI:6901905
                                                                                                                                                                                                                                                                 AV398253
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(5' -> 3')
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Unpublished (2000)
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Bombycoidea; Bombycidae; Bombyx.
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                 National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
                                                                                                                                                                                                   Bombyx mori
                                                                                                                                                                                                                                                                             Bombyx mori cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: .Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mita,K., Morimyo,M., Shimada,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 6 hr
189 c 205 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV060300"
                                                                                                                                  1 to 693)
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75.8%;
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No. 6.3e+02;
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                                                                                                                 Okano, K.
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Glossata; Ditrysia;
               Japan
                                                                                                                                                              oda; Insecta; Pterygota;
Glossata; Ditrysia;
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AV398450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV398450 701 bp. mRNA linear AV398450 Bombyx mori ovary BmNPV infected; 2 hr at Bombyx mori cDNA clone NV021825 T3, mRNA sequence AV398450
1 CGGTGTACTCACCGTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                          Contact. ....
Genome Research Group
National Institute of Radiological Sciences
----- 4-9-1, Inage, Chiba 263-8555, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Endopterygota; Lepidoptera; Glos
Bombycoidea; Bombycidae; Bombyx.
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(5' -> 3')
                                                                                                                                                                                                                                                                                        Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/>,</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombyx mor1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mita, K., Morimyo, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV398450.1
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<http://www.ab.a.u-tokyo.ac.jp/silkbase/>,
                                                                                                                                                                                                                                                                                                                                                          method:uni-directional,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domestic silkworm.
                                                              Similarity
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                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                      kmita@nirs.go.jp
                                                                                                                    /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr
/dev_stage="214 g 164 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr
193 c 212 g 160 t
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/db_xref="taxon:7091"
/clone="NV021292"
                                                                                                                                                                                     inoculation*
                                                                                                                                                                                                                /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV021825"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inoculation"
                                                                                                                                                                                                clone_lib="Bombyx mori ovary BmNPV
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                                                            61.2%;
75.8%;
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                                                            Score 20.2; DB 10
Pred. No. 6.4e+02;
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Pred. No. 6.3e+02;
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Glossata; Ditrysia;
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                                              Indels
                                                                        Length
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                                                                            701;
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                                              Gaps
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REFERENCE
AUTHORS
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AV398164
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                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                               DEFINITION
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AUTHORS
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ORGANISM
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VERSION
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AV401743.
                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                   Loca.
National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
                                                                                                                                                                                                                         AV398164 Bombyx mori ovary BmNPV infected;
Bombyx mori cDNA clone NV021198 T3, mRNA se
                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                               Contact: Mita K
                                                           Bombyx mori cDNA
Unpublished (2000)
                                  Genome Research Group
                                                                                                                                                                                                   (¥398164.1 GI:6901816
                                                                                                                ombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV401743 Bombyx mori-
clone heS00104 T3, m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project-'Silkworm Genome Program in MAFF, and Research for the ruture Program in JSPS'. see 'SilkBase', for whole ESTdb.
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                    ta, K., Morimyo, M.,
                                                                                                                            optera; Endopterygota;
                                                                                                                                                                                                                                                                                                                             CGCGGAACTCTCCGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enome Research Group
Mational Institute of Radiological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omestic silkworm.
                                                                                                                                                                       estic silkworm.
                                                                                                      (bases 1 to 735)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l: kmita@nirs.go.
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Bombyx mori C108 spinning stage day-0"/sex="female/male mixed"
/cell_type="hemotyte"
/dev_stage="spinning stage day-0"
201 c 211 g 163 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="heS00104"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain="C108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               61.2%;
75.8%;
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                                                                                  Shimada, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arthropoda; Hexapoda; Insectota; Lepidoptera; Glossata;
                                                                                                                                                                                                                                                                                                                         TGGCCCACTATCGC
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                                                                                                                            Lepidoptera;
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spinning
                                                                                 Okano, K. and Maeda, S
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.4e+02;
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                                                                                                                       Insecta; Pterygota;
ssata; Ditrysia;
                                                                                                                                                                                                                                   linear EST 05-FEB-200; 2 hr after inoculation
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ssata; Ditrysia;
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Indels

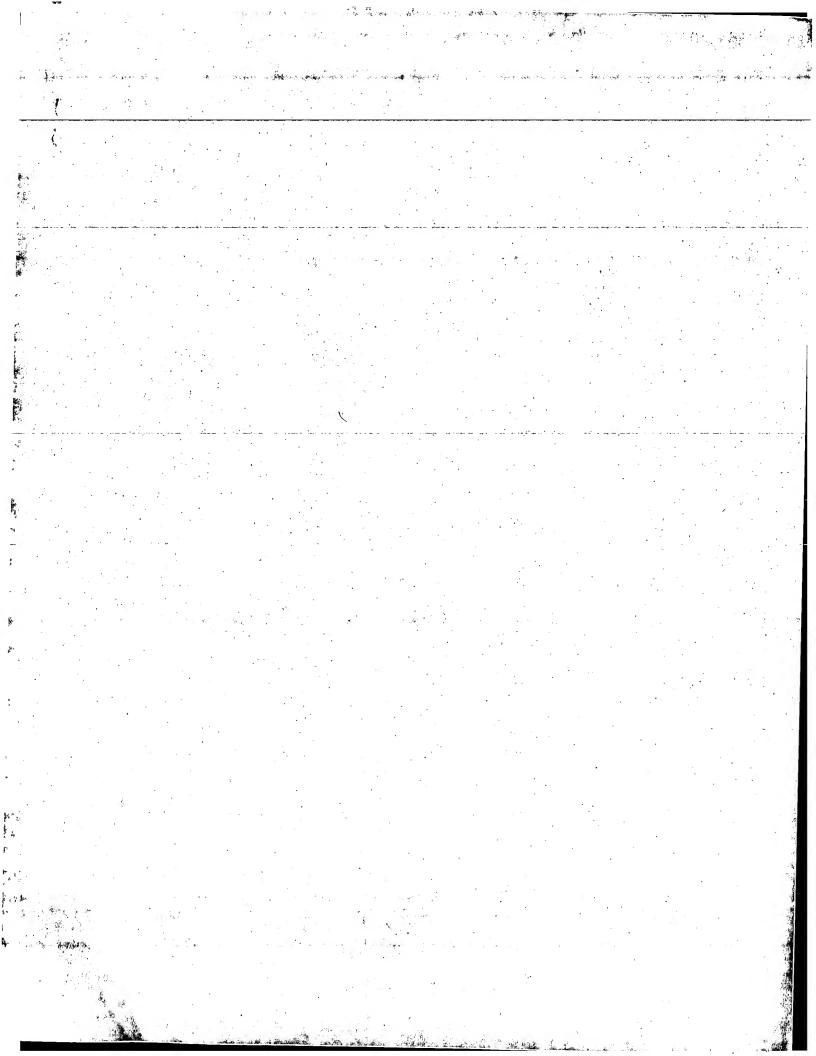
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Gaps

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BASE COUNT
ORIGIN
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AV398482
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Best Local S
Matches 25
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                      Similarity
                                                                                                                                                                                                                                          Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, Location/Qualifiers
                                                                                                                                                                                                                                                                                                              method:uni-directional, sequence direction:sequenced
(5' -> 3')
                                                                                                                                                                                                                                                                                                                                         Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV398482 Bombyx mori ovary BmNPV infected; 2 hr af Bombyx mori cDNA clone NV021859 T3, mRNA sequence.
                                                                                                                                                                                                                                                                          Project='Silkworm Genome Program in MAFF, uture Program in JSPS'. see 'SilkBase',
                                                                                                                                                                                                                                                                                                                                                            Anagawa 4-9-1
                                                                                                                                                                                                                                                                                                                                                                        Genome Research Group
National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bombycoidea; Bombycidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bombyx mori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domestic silkworm.
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Future Program in JSPS'. see 'SilkBase',
<a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/>,</a>
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method:uni-directional,
(5' -> 3')
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 790)
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                                                                          /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2
/dev_324 c 235 g 181 t
                                                                                                                                                                              /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV021859"
                                                                                                                                                          /clone_lib="Bombyx mori ovary BmNPV infected;
                                                                                                                                                   noculation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="BMN cultured cell"
/dev_stage="BMNPV infected; 2
205 c 221 g 173 t
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/db_xref="taxon:7091"
/clone="NV021198"
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                    61.2%;
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75.8%;
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Score 20:2; DB 10;
Pred. No. 6.6e+02;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimada,T.,
                                                                                                                                                                                                                                                                                                                                                     Radiological Sciences
Chiba 263-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20.2; DB 10;
Pred. No. 6.4e+02;
D; Mismatches 8;
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Search completed: July 11, 2003, 02:25:28 Job time: 600.333 secs



BF427489 df89a04.y BB655806 BB655806 BH728734 BONNE79TR AL193347 Tetracdon AL422644 T3 end of BG399084 60244075 BB098595 BB098595 BB098595 BB098595 AQ368408 HS\_5039\_A AQ368431 HS\_5039\_A AQ368431 HS\_5039\_A AQ368431 HS\_5039\_A AQ368431 HS\_5039\_A AQ368431 HS\_5039\_A AQ368431 HS\_5039\_A AQ368431 HS\_5039\_A

AL254631 Tetraodon AL342711 Tetraodon BC250312 602362445 BC848013 102462080 AZ387734 1M0147C22 W98110 mg25c04.r1

BQ602301 MI-P-HO-a BF099337 601751722

BQ328104 MR1-RT007 BG383655 301851 MA AV244148 AV244148

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Title:
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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em_estov:*
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AA432035 zw80e02.r
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                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                    354 bp mRNA linear EST 13-JUN-2001
PMO-ET0208-030201-005-c04 ET0208 Homo sapiens cDNA, mRNA sequence.
BI014511.
BI014511.1 GI:14418582
                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                Nagai, M.A., da Silva, W. Jr., 2ago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Sares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               1 (bases 1 to 354)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S.,
                                                                                                                                                                                                                                                                              EST.
                                                                                                               sequence tags
                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                      Simpson, A.J.
 Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                  human.
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66
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AZ892007 RPCI-24-1 BG154115 421 L1N01 BE681567 179279 MA BH687462 BOMGN17TR B0339788 RC1-NN023 AT341663 QQ95f06.x

Briones, M.R.,

Paulo-SP

BE047681 tz40e06.y BB222109 BB222109 AZ892007 RPCI-24-1 BG154115 421 L1N01

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Gaps

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clone

IMAGE:5578052

linear

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High quality sequence start: 18
High quality sequence stop: 551.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Fissue Procurement: ATCC
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National Institutes of Health, Mammalian
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601450002F1 NIH_MGC_65
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 912)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=pMO&t2-pMO-ETO208-
030201-005-c04&t3=2,001-02-03&t4-1)
                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                 und through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCTCAGTACTTGGTCATCTTCTCT 38
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Location/Qualifiers
                                                                                                                                                                                                                                                           LLAM9578 row: d column:
                /Clone_lib="NIH_MCC_65"
/tissue_type="adenocarcinoma"
/lab_host="pH10B (phage_resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1:
Site_2: SalI; Cloned unidirectionally. Primer: Ol
Average insert size 1.8 kb. Library constructed
                                                                                                                                      /clone="IMAGE:3853777"
                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                       ′organism="Homo sapiens"
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/db_xref="taxon:9606"
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sapiens cDNA clone
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Best Local
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                                                                                              AV047458 Mus musculus adult C57BL/6J testis
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Mus musculus
                                                  AV047458.2 GI:4867123
                                                                        AV047458
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                                                                                     1700067016,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium |
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informati
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5', mRNA sequence.
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1 (bases 1 to 1008)
NIH-MGC http://mgc.nci.nih.gov/
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Plate: LLAM12332 row: h column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMv-SpORT6;
Site_2: Sall; Cloned unidirectionally. F
Average insert size 2 kb. Library const
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Technologies."
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/db xref="taxon;9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="NIH_MGC_72"
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ches 5;
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Matches Best Local Query Match

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Conservative

BASE COUNT

116 a

FEATURES

source

COMMENT

TITLE JOURNAL AUTHORS

Inpublished (1999)

ontact: Robert

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FEATURES

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musculus cDNA clone

EST 23-NOV-1999

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                                                                                                                                                           296
zw80e02.rl Soares_testis_NHT
5', mRNA segmence
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 296)
                                                          Homo sapiens
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                                                                                                                                          5', mRNA sequence.
AA432035
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RIKEN Mouse ESTs
Unpublished (1999)
                                                                                                                     AA432035.1 GI:2115743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptional sequencing: A method for DNA sequencing upolymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 Please visit.our web site (http://genome.rtc.riken.go.jp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                 numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@rtc.riken.go.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 280)
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l: 81-298-36-9145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptors (Pharmacia), digeste
the Not I and Eco RI sites of
RNA provided by Dr. Minoru Ko,
constructed and normalized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mus musculus adult C57BL/6J testis"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="1700067016"
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/dev_stage="adult"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                         68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into I and Eco RI sites of the modified pT7T3 vector.
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Pred. No. 5.1e+02;
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                                                                                                                                                                                  cDNA clone
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                                                                                                                                                                                              linear
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                                                                                                                                                                                  IMAGE: 782522
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COMMENT
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AUTHORS
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ORGANISM
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AA758968/c
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Best Local S
Matches 24
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                                                                                                                                                                                                                                                                                                                                             human.
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361 bp mRNA linear EST 31-Di ai29a05.sl Soares_testis_NHT Homo sapiens cDNA clone 1344176 similar to contains Alu repetitive element: mDNA commandation AN758968
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                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative full length read
The vector to vector length is 349
Seg primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillier, L., Allen, M., Bowle Kucaba, T., Lacy, M., Le, N.,
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can b found through the I.M.A.G.E. Consortium/LLML at:
                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                    cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                    Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "91 c 90 g 64 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Pharmacia),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; list strand
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/clone_lib="Soares_testis_NHT"
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Pred. No. 5.2e
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.2e+02;
                                                                                                                                                                                                                                           Genome Anatomy Project (CGAP),
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                                                                                                                      Fatima Bonaldo
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                      i (bases I to 385);
Ricaba, T., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2193906.sl Soares_testis_NHT Homo sapiens cDNA clone
                                                                                                                                                                                                                MAGE Consortium (info@image.llnl.gov) f
eq primer: -41ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
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                                                                                                                                                                                                                                                                                       314 286 1800
314 286 1810
                                                                                                                                                                                                                                         1: est@watson.wustl.edu
clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                  quality sequence stop:
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                polylinker;
                                                                                            /organism="Homo sapiens"
/db_xref="GDB:5926475"
/db_xref="taxon:9606"
/clone="IMAGE:729946"
     note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
                                                'lab_host="DH10B"
                                                                                  clone.
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 98 c 99 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="13,44176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                            _lib="Soares_testis_NHT"
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.6e+02;
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MAGE:729946
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JOURNAL
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                                                                                                                                                                                                                                                                                           High quality sequence stop: 480. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                      Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Schellenberg, K., Steptoe, M., Tan, F., Theising, B., T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Uppublished 1997
                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Allen, M. Kucaba, T., Lacy, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 509)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                   est@watson.wustl.edu
and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

174.c 146 g 107 t
                                                                /db_xref="taxon:9606"
/clone="IMAGE:729946"
                                                                                                                                                                          Lab_host-"DH10B"
                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                       /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:5926475"
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Query Match
Best Local Similarity

68.0%;

Score 20.4; DB 9; Pred. No. 6.5e+02;

Length 509;

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ACCESSION
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BQ328104
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AUTHORS
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                                                AUTHORS
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nammana...
1 (bases 1 to 542)
1 (bases 1 to 542)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mays cDNA, mRNA sequence.
                                                                                                                             EST
                                                                                                                                       BQ328104
MR1-RT0079-151200-003-b02
BQ328104
BQ328104.1 GI:20946200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Lili
clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae;
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                                                                                     Eukaryota;
                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                           TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
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                                                                                                                                                                                                                                                                                                     Conservative
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486096 row: E column:
                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leaf primordia"
/dev_stage="P7-P11 leaf"
/lab_host="E_coli Xi1-Blue MFR/"
/note="Organ: shoot; Vector: Lami
library."
92 c 146 g 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:4577"
/clone_lib="486.- leaf primordia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="2ea mays"
cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                     Metazoa;
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                                                                      Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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yta; Liliopsida;
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1; Poales; Poaceae;
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aceae; PACC
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                                                                                                                                                                 and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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EST discovery in swine Unpublished (2000) Contact: Smith TPL
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR1&t2=MR1-RT0079-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetic
Ludwig Institute for Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human
                                                                                                                                                                                                                                                     Fahrenkrug, S.C.,
                                                                                                                                                                                              Design and use of two
                                                                                                                                                                                                                                   Stone, R.T., Heaton, M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151200-003-b02&t3-2000-12-15&t4-1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
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Prof. Antonio Prudente 109, 4 and
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                                    smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Organ: kidney_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue mRNA and cDNA amplification
low stringency conditions."
194 c 136 g 119 t 3
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                   Freking, B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
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Pred. No. 6.6e+02;
0; Mismatches 6;
                                                                                                                                                                                            pooled
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Laegreid,W.W.
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RESULT 12
AV244148/c
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FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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Best Local
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                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                      sequencing
                                                                                                                                                                                                                                                                                                                                                                                        Sciences Center(GSC) Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                          RIKEN integrated sequence analysis (RISA) system--384-format equencing pipeline with 384 multicapillary sequencer. Genome
                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciure
1 (Dases 1 to 705)
Arakawa, T., Carninci, P., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FORWARD: AGGAAACAGCTATGACCAT
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81-45-503-9216
                                                                                                                                          Kawai, J., Okazaki, Y., Muramatsu,
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                                                                                                                                                    Genome Res. 10 (10), 1617-1630 (2000)
K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
ki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
                                                                ng pipeline with
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205 c 121 g 176 t
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/clone_lib="MARC 1PIG"
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                                                                                                                                                                                                                                                                                                                                                                           Tsurumi-ku,
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                                           Y., Shibata, K.,
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Pred. No. 6.8e+02
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                                                                        multicapillary sequencer. Genome Res.
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d, 0 day neonate head
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                                     Itoh, M., Carninci, P.
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                                                                                                                                                                                                                                                                                                                                                                         Kanagawa
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                                                                                                                                                                                                                                                                      Shibata, K., Itoh
                                                                                                                                      Kira, A.
                                                                                                                                                                                                                                                                                                                                                                       230-0045,
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345 · TGGTCTCCTTACTTGGTCTTCACACCTTCT
                                                                        1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encyclopedia: rear came Genome Res. . 11 (2 nonredundant cNA library. Genome Res. . 11 (2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site
                                                                                                                                                                                                                                                                                                                                                                               209
                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                3']. cDNA was cloned into the xhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk exform. Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primed with a primer [5' GAGAGAGAAGAAGCTCTTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Genomic Sciences Center and Genome - The Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Contr
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/note="si+-
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/dev_stage="0 day no
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/clone="4831428F09"
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/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                           GSS; genome survey sequence. Tetraodon nigroviridis.
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                                   Tetraodon.
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                                                                     Neoteleostei;
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Roest-Crollius,H.,

Jaillon, O.,

Dasilva,C.,

Bouneau, L.,

Fisher, C.

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RESULT 14
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                                                                                                                                                                                                           Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C. Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis usir Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                            GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
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2 (Dases 1 to 800)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Rouneau.L., Billault, A., Quetier, F., Saurin, W., Bernot,
 Submitted (12-APR-2000)
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Direct Submission
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Tetraodon nigroviridis DNA sequence
                                                                                                                         Weissenbach,
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Roest-Crollius, H., J
                                                                                                                                                                                              Unpublished
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                                                                                       freshwater pufferfish
                                                                                                                                          Bouneau, L., Billault, A.,
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/db_xref="taxon:99883"
/clone="045115"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert St
                                                                                                                                                                                                                                                                                                                   High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
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LLAM10289 row: 1 column:
                                                                                                     /tissue_type="adenocarcinoma, cell line"
/lab_host="DBH0B (phage-resistant)"
/note="Organ: liver; Vector: pcwv-SpoRT6; Site_1
Site_2: Sall; Cloned unidirectionally; oligo-dT
saverage insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Techn
Note: this is a NIH_MGC Library."
a 401 c 323 g 186 t
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/note="Genoscope sequence
/note="Genoscope sequence
256 c 262 g 275
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/db_xref="taxon:99883"
                                                                                                                                                                                                                                      /clone="IMAGE:4470994"
/clone_lib="NIH_MGC_90"
                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                      Site_1: NotI; igo-dT primed.
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nigroviridis
                                                                                                                                        Technologies
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482 TGGTCTCACTCCTTGGACTTGTCACCTTGT 511

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
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length: 2000000000
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                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           July 10,
                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*
1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
66.7
66.7
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/FBTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                              Length DB
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US-08-2
US-08-2
US-08-2
US-08-2
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US-08-256-568B-56
US-08-256-568B-57
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PCT-US95-07671
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; LOCATION:
US-08-690-495-26
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US-08-690-495-26
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                            Matches
                                                                                           FEATURE:
                                                                                                                                                                                                                 NAME:
1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
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ALIGNMENTS

## GENERAL INFORMATION: APPLICANT: Zhang, INFORMATION FOR SEQ ID NO: APPLICATION NUMBER: US/OI FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: FasSEQ Version #1.5 CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 120 base pairs TELECOMMUNICATION INFORMATION: TELEPHONE: 212-408-2597 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MOLECULE TYPE: DNA (genomic) NUMBER OF SEQUENCES: 4 APPLICANT: Zhang, David Y., Brandwein, Margaret TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD: TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION TYPE: ....STRANDEDNESS: SI REGISTRATION NUMBER: TELEFAX: REFERENCE/DOCKET NUMBER: COMPUTER: COUNTRY: STREET: ADDRESSEE: 3 26, 55 40. 587.6924 l Similarity 33; Conserv 10112-0228 nucleic acid MacLeod, Janet Application US/08690495 120 base pairs E: Brumbaugh, Graves, 30 Rockefeller Plaza 212-765-2519 USA Conservative misc\_feature 1..120 IBM PC compatible single 66.7%; 97.1%; US/08/690,495 35,263 0, 29545-A-PCT/USA-A Score 22; Pred. No. Mismatches Donohue & Raymond 0 DB 2; Length 120; Indels ' METHOD (HSAM) 1; Gaps

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1;

CGGTGTACTCACCGGTTCCGCAGACCACTATGGC 97

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PCT-US95-07671-26
                                                                                                                                                                           Sequence 26, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                               Matches
                   COMPUTER
                                                                                                                                      TITLE OF
                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-765-2519
FORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 OLECULE TYPE:
      MEDIUM TYPE:
                                           COUNTRY
                                                          STATE:
                                                                        CITY:
                                                                                    STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MACLEOO, Janet M.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELECOMMUNICATION INFORMATION: TELEPHONE: 212-408-2597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NERAL INFORMATION:
APPLICANT: Zhang, David Y., Brandwein, Margaret
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                               LOCATION:
90-494-26
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                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                        |Similarity 97.1
|33; Conservative
READABLE FORM:
TYPE: Floppy disk
                                                                                                                                  INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARE: FasSEQ Version #1.5
APPLICATION DATA:
                             0112-0228
                                                                    New York
                                                                                                                                                  INVENTION:
                                                                                                                                                                                                                                                CHARACTERISTICS:
1: 120 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY: USA
10112-0228
                                                                                                                                                                                   Application PC/TUS9507671
                                                         ΝY
                                                                             30 Rockefeller
                                           USA
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                                                                                                                                                              Zhang, David Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 Rockefeller plaza
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                                                                                                                                                                                                                                                                                                                                                                          1..120
                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brumbaugh, Graves, Donohue & Raymond
                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                      DETECTION OF INFECTIOUS PATHOGENS
                                                                                                                                                                                                                                                                                                                    66.7%;
97.1%;
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                                                                                      Graves, Donohue & Raymond
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                                                                                                                                                                                                                                                                                                                 Score 22; DB 2;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29545-A-PCT/USA-B
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                     0;
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RESULT 4
US-08-690-495-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atent No.
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INFORMATION FOR SEQ ID NO:
                                                   TELEPHONE: 212-408-2597
                                                                                                                                                                                                             SOFTWARE: FasSEQ Version #1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: MacLeod, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                    NAME: MacLeod, Janet M. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Zhang, David Y., Brandwein, Margaret
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD: (HSAM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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CURRENT APPLICATION DATA:
                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 1.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seide, Rochelle K.
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: " PCT/US95/07671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 CGGTGTACTCACCGGTTCCGCAGACCACTATGGC
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                                                                                                                                                                                                                                                                                                                    10112-0228
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30 Rockefeller Plaza
                                  212-765-2519
                                                                                                                                                                                                                                                                                                                                     USA
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97.1%;
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                                                                                29545-A-PCT/USA-A
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Pred. No. 0.27;
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Gaps

ENGTH:

1: 145 base pairs nucleic acid

MOLECULE TYPE: DNA (genomic)

NAME/KEY:

misc\_feature 1..145

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            PCT-US95-07671-18

Sequence 18, Application PC/TUS9507671

GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                    Matches
                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY TYPE: FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
MEDIUM TYPE: IBM PC compatible
MEDIUM TYPE: IBM PC compatible
MEDIUM TYPE: IBM PC compatible
MEDIUM TYPEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 594239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FasSEQ Version #1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                             ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          E: MacLeod, Janet M. ISTRATION NUMBER: 35, ERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 CGGTGTACTCACCGGTTCCGCAGACCACTATGGC 105
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                                                                                                                        1. CGGTGTACTCACC-GTTCCGCAGACCACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                                                                        CGGTGTACTCACCGGTTCCGCAGACCACTATGGC 105
                                                                                                                                                                                                                                                                                                                                  nucleic acid
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                              : 212-408-2597
212-765-2519
Zhang, David Y.
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                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David Y., Brandwein, Margaret
H: NUCLEIC ACID AMPLIFICATION METHOD:
H: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)
                                                                                                                                                                                66.7%;
97.1%;
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Pred. No.
                                                                                                                                                                                Score 22;
Pred. No.
                                                                                                                                                                 Mismatches
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0.28;
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RESULT 7
US-08-256-568B-55/c
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Matches 33
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5:
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-408-2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seide, Rochelle K.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION:
                                                                                                                                                                                                                                               ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                PPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TILE OF INVENTION: PROCESS FOR TYPING OF HCV
TILE OF INVENTION: ISOLATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 33; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 1..145
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                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                 ADDRESSEE:
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10112-0228
                                                                                                                                                                             NEW YORK
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30 Rockefeller Plaza
                                                                                                                                                               USA
                                                                                                                                                                                                                  600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212-765-2519
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                                                                                                                                                                                                                                                                                                                                   MAERTENS, GEERT; STUYVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                BIERMAN & MUSERLIAN
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97.1%;
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Pred. No.
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US-08-256-568B-55
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  PRIOR APPLICATION DATA:
APPLICATION NITMENT
                                                      FILING DATE: 26-NOV-PRIOR APPLICATION DATA:
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
FILING DATE: 26-NOV-1993
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                             CURRENT
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                           NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
                          APPLICATION NUMBER: EP/93/402,129.6 FILING DATE: 31-AUG-1993
                                                                                                              APPLICATION NUMBER: US/08/256,568B FILING DATE: 18-JUL-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                 STREET:
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APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARPLICATION DATA:
APPLICATION NUMBER: PCT/P
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POSITION: 5' untranslated region
                                                                                                                                                      APPLICATION DATA:
                                                                                                                                                                                                                                                                    NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                              THIRD AVENUE
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                                                                                                                                                                                                                                                                                                                                                           PROCESS FOR TYPING OF HCV
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EP/92/403,222.0
                                                                                  PCT/EP93/03325
                                                                                                                                                                                                                                                                                                                                                                                       GEERT!; STUYVER, LIEVEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP/93/402,129.6
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Pred. No.
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Gaps

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US-08-256-568B-57/c
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US-08-256-568B-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                      APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT IMPORAATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIAL 9581
POSITION IN GENOME:
REFERENCE/DOCKET NUMBER: 410
TELECOMMUNICATION INFORMATION:
                                                                                                                                                FILING DATE: 26-NOV-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO TITLE OF INVENTION: PROCESS FOR TYPING OF HCV TITLE OF INVENTION: ISOLATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
                                REGISTRATION NUMBER:
                                                                                                                                                              APPLICATION NUMBER: PCT/
FILING DATE: 26-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                               10016
                                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
                                           CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, Application US/08256568B 5846704
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                                                                                                                                                                                                                                                                                                                                                                                                      600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                            Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
ilarity 97.1%;
Conservative
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                            19,683
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               410.004
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Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
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TELEPHONE:

(212)

661-8000

(212) 661-8002 OR SEQ ID NO:

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RESULT 10
US-08-256-568B-58/c
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; MAP POSITION: 5' untranslated region
US-08-256-568B-57'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                          TELEFAX: (212) 661-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quence 58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26:NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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                                                                   MOLECULE TYPE:
                                                                                                                                                                                     TELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORRESPONDENCE ADDRESS:
                                                 MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP/93/402,129.6 FILING DATE: 31-AUG-1993 RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
DSITION IN GENOME:
MAP POSITION: 5'untranslated region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1:
CLASSIFICATION:
                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/256,568B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
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NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8, Application US/08256568B 5846704
                                                                                                                                                                                                                                                                                 ATION NUMBER: EP/9
DATE: 27-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTGTACTCACCGGTTCCGCAGACCACTATGGC 40
                                                                                                                                                                                                                                                   CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSSAU, RUDI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAERTENS, GEERT; STUYVER, LIEVEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                linear
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                                                                                              single
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                                                                                                                                                                       661-8002
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97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROCESS FOR TYPING OF HCV
                                                                                                                                                                                                                                                                                                 EP/92/403,222.0
                                                                                                                                                                                                                                    19,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAN HEUVERSWYN,
                                                                                                                                                                                                                         410.004
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Pred. No. 0.28;
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                               Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                 TELEFAX: (212) 661-8002 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No. 5846704
ENERAL INFORMATION:
                                                                                            POSITION IN GENOME:

OSTRON: 5' untranslated region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWAKE: CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/256,568B
                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                        IMMEDIATE SOURCE:
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                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27-NOV-1992
TTORNEY/AGENT INFORMATION:
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hes 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/
FILING DATE: 26'-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                        ropology:
                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEW YORK
                                                                                                                                                                                                                nucleic acid
   CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                                                                                                                                                                                                                                                                                                                           CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08256568B
                                                                                                                                          be82 (also referred to as be99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROSSAU, RUDI; VAN HEUVERSWYN, H
VENTION: PROCESS FOR TYPING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAERTENS, GEERT; STUYVER, LIEVEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIERMAN & MUSERLIAN
                                                                                                                                                                                                                                                                                                 (212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-1994
                                                                                                                                                                        CDNA
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                                                                                                                                                                                                                                                                                                                                                                                         MBER: EP/92/403,222.0
27-NOV-1992
                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                661-8000
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                                               66.7%;
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                                                                                                                                                                                                                                                                                                                            410.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 2; Pred. No. 0.28; 0; Mismatches
                                               Score 22; DB 2; Pred. No. 0.28;
                                 Mismatches
                                   0;
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                                                            Length 177;
                                 Gaps
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US-08-256-568¤-63/c
                                                                   Sequence 63;
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                       Query Match
Best Local
                                  GENERAL INFORMATION:
                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
        APPLICANT:
                                                                                                                                                                                                                                                                             POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                CLONE: be90
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
RELECOM/UNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP/9
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHASSIFICATION DATA:
RIOR APPLICATION NUMBER: PCT/ED93/03325
PTLING DATE: 26-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN; NPPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
NITLE OF INVENTION: PROCESS FOR TYPING OF HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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                                                                                                                                   1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                    3) Application US/08256568B
5846704
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                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATION NUMBER: EP/92/403,222.0
DATE: 27-NOV-1992
/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARLES A. MUSERLIAN
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MAERTENS, GEERT; STUYVER, LIEVEN; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEW YORK
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CAN NUMBER: EP/93/402,129.6
                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                            untranslated region
                                                                                                                                                                                                66.7%; Score 22; DB 2; 97.1%; Pred. No. 0.28; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/256,568B
                                                                                                                                                                                                  0
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RESULT 14
US-08-256-568B-64/c.
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Best Local s
Matches 33
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                                                                                                                                         Patent No.
                                                                                                                                                     Sequence 64,
                                                                                                                         GENERAL INFORMATION:
                                                                                       APPLICANT: N
                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      CLONE: be91
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
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                                             NUMBER OF SEQUENCES:
                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP/9
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
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CURRENT APPLICATION DATA:
US/08/256,568B
   STREET:
                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                       73 CGGTGTACTCACCGGTTCCGCAGACCACTATGGC 40
                                                                                                                                                                                                                                           1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
                                                                                                                                        4, Application US/08256568B 5846704
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: single
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E: BIERMAN & MUSERLIAN 600 THIRD AVENUE
                                                                  MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUG
VENTION: PROCESS FOR TYPING OF HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 base pairs
                                                                                                                                                                                                                                                                                      Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : (212) 661-80
(212) 661-8002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                        ISOLATES
                                                                                                                                                                                                                                                                                                   66.7%;
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                                                                                                                                                                                                                                                                                                  Score 22; DB 2;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                   Mismatches
                                                                       HUGO
F HCV
                                                                                                                                                                                                                                                                                   Ō,
                                                                                                                                                                                                                                                                                                           Length 177;
                                                                                                                                                                                                                                                                                 Indels
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Gaps

NEW YORK

CURRENT APPLICATION DATA:

OPERATING SYSTEM:

IBM PC compatible.
SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

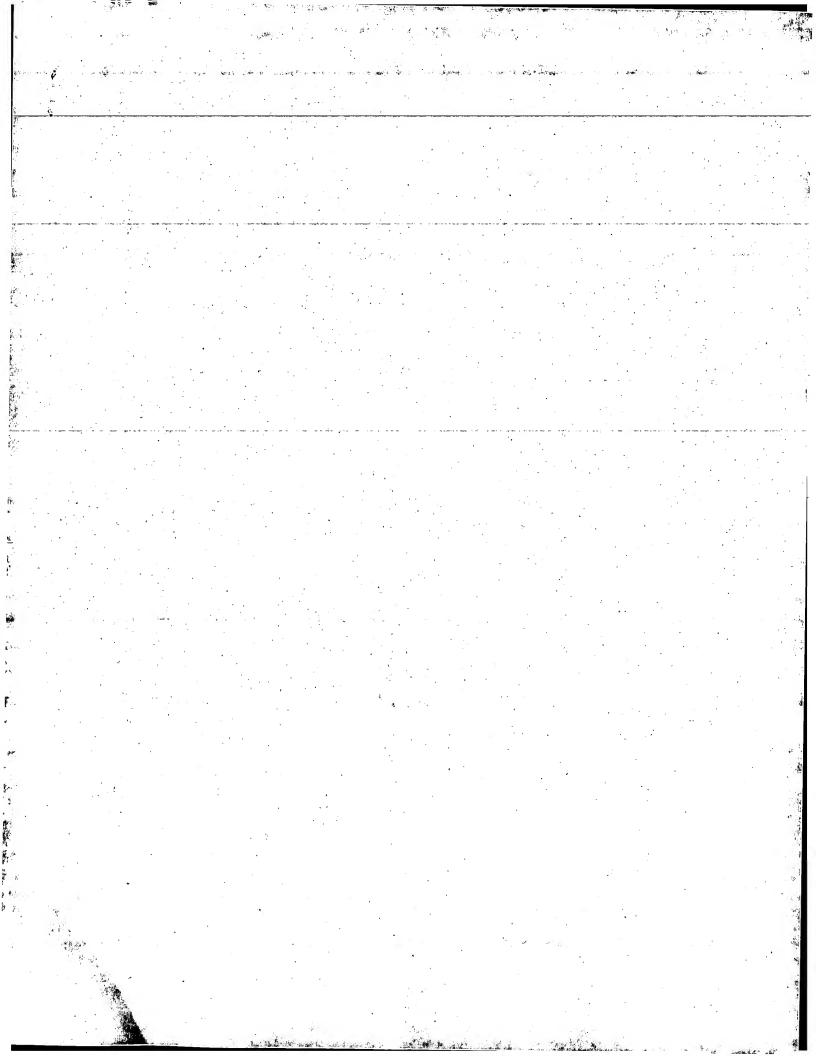
Floppy disk

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RESULT 15
US-08-256-568B-65/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Sequence 65, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOSTEM: PC-DOSTMS-DOS
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PRIOR APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME: MAP POSITION: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                               ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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PRIOR APPLICATION UNMBER: PCT/EP93/03325
                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                            PPLICANT:
FRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 26+NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 410.004
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                                                SOFTWARE:
                                                                                                                                                                                    STREET:
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                                                                                                                                         OUNTRY:
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                                                                                                                                                    NEW YORK
                                                                                                                            10016
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ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
VENTION: PROCESS FOR TYPING OF HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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97.1%;
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Pred: No. 0.28;
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US-08-256-568B-65
                                                     Query Match
Best Local Similarity
Matches 33; Conserv
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                                                                                                                                          CLONE: be93
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP/9
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
EP/92/403, 222.0
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 26-NOV-1993
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73 CGGTGTACTCACCGGTTCCGCAGACCACTATGGC
                1 CGGTGTACTCACC-GTTCCGCAGACCACTATGGC 33
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                                                                              Score 22; DB 2; pred. No. 0.28;
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Search completed: July 10, 2003, 20:27:12 Job time: 15.7573 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                          Score
                           \begin{smallmatrix}3&5&3&5\\3&5&5\end{smallmatrix}
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Copyright (c) 1993 - 2003 Compugen Ltd.
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BB854666 AW473754 AL043622 AQ160900 BI689033	AAG33661 AG008799 BI151067 CNS0091P EM810632 BM459695 BE616401 BM921090 BF508846 BE424949 TA164C12Q AQ538955 AZ113390	AA172136 BB628805 BIT53642 BMT38887 BE888083 BIT65955 CNS0091P BF306437 BC014080 AA631550 AA69278 BJ48431550 AA69278 BJ484211 BJ485696 AV945501 BJ483757 BJ483019 BJ482842 BG031227 AA633661
14390 RFC1-23- 5466 BBS4666 73754 ha78906. 3622 DKFZP434H 60900 nbxb0006 89033 60331332	33661 a 008799 1008799 1051067 1053013 810632 810632 8106401 616401 616401 538946 474944 1133990	72136 zp29e06 628805 BB6288 153642 FC2871 738887 K-EST0 888083 601511 738887 601511 765955 603047 053013 Drossop 306437 601893 014080 Homo s 014080 Homo s 931550 zw78d09 69278 zm12a03 484211 BJ4854 4845501 AV9455 945501 AV9455 945501 AV9459 483757 BJ4837 483757 BJ4837 483757 BJ4838 684127 6022141 33661 acl5h12

## ALIGNMENTS

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source	FEATURES					:		COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			•	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AL798317/c
1534 /organism="Silurana tropicalis"	constructed by Aaron M. Zorn. Location/Qualifiers	This sequence is from a Xenopus Gene Collection (XGC) library	Sequencing primer: P1CSP6	Sanger Xenopus tropicalis EST project 2001	Email: trop@sanger.ac.uk	Hinxton, Cambridgeshire, CB10 1SA, UK	Sanger Centre	Contact: Taylor R	Unpublished (2001) .	Sanger Xenopus tropicalis EST project 2002	Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.	1 (bases 1 to 534)	Xenopodinae; Silurana.	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Silurana tropicalis	western clawed frog.	EST.	AL798317.1 GI:21584021	AL798317	mRNA sequence.	AL798317 XGC-neurula Silurana tropicalis cDNA clone TNeu133m07 5',	AL798317 534 bp mRNA linear EST 27-JUN-2002	

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BASE COUNT
ORIGIN .
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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Best Local
source
                 Local
                       Similarity
                                                                                                                                                                                                                                                                     constructed by Aaron M
                                                                                                                                                                                                                                                                                                     mail: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project :
TROPICALIS_SEQUENCE_ID: TGas026a22.sp6
                                                                                                                                                                                                                                                                                                                                                                               Sanger Xenopus tropicalis
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ēukaryota; Mētazoa; Chordata; Craniata; Vej
Āmphibia; Batrachia; Anura; Mesobatrachia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTCCGGAGAAGGATGCTGAACGCTGGATAGAGCGGGGCTGCGGGGTATTTGCACGGCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATGGCGGTACTCACGGCACAGGGCATCCAGCAGGGGCACGGAGACTGGGCGCAGCGGGA 254
                                                                                                                                                                                                                                                                                                                                                                     nger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105
                                                                                                                                                                                                                                                                 sequence is from a Xenopus tructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                   bases .1
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                                                                                                         /lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI;
was oligo dT primed from 5ug of poly A+ RNA from 5tg
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligat
                                                                                                   into pcs107
                                                                                                                                                                                                                                                                                                                                                  Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                               /dev_stage="gastrula (stages 10.5-13 mixed)"
                                                                                                                                                                                 /clone_lib="XGC-gastrula"
                                                                                                                                                                                                 /clone="TGas026a22"
                                                                                                                                                                                                              /organism="Silurana tropicalis"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pCS107; Site_1: EcoRI; Site_2: Not was oligo dr primed from 5ug of poly A+ RNA from EcoRI-NotI cut cDNA was then ligated into pCS107 EcoRI at the 5' end and NotI at the 3' end."

1/1 c 175 g 84 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="XGC-neurula"
/dev_stage="neurula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lab_host="Escherichia coli DH10B"
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                  Score
Pred.
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       148
                        137 CAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGACTGCTAGC 187
                                                                                                             268 CATGGCGGTACTCACGGCACAGGGCATCCAGCAGGGGCACGGAGACTGGGCGCAGCGGGA
                                                      208 TGCTCCGGAGAAGGATGCTGAACGCTGGATAGAGCGGGGCTGCGGGGTATTTGCACGGCT
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                                                                                                                                                                                   86,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
CTAGCCCTTACACTCCCGGGGATTGCAGCCTACTGCAGCCGGGCTTGTGGC
                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu021f04.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Huckle E
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huckle, E., Taylor, R., Ash
Sanger Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis
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AL636391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia; Batrachia; Anura; Mesobatrachia;
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                                                                                TGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGGGTCCTTTCTTGGAT
                                                                                                                                          86; Conservative
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                                                                                                                                                                                                                                                was oligo dT primed from Sug of poly A+ RWA from neurula EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                      /clone="TNeu021f04"
/clone_lib="XGC-neurula"
                                                                                                                                                                                                                                                                                                           /lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: Ecol
                                                                                                                                                                                                                                                                                                                                          'dev_stage="neurula
                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:8364"
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Pred. No.
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RESULT 4
AL784104/c
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BE249938/c
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 928)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                     EST.
                                                                                                                                                  mRNA sequence.
                                                                                                                                                                    600942989F1 NIH_MGC_15
                                                                                                                                                                                       BE249938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. Sanger Xenopus tropicalis EST project 2002
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AL784104.1 GI:21569808
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                                                                Homo sapiens
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http:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XGC-gastrula Silurana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/lab_host="Scherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
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/clone_lib="XGC-gastrula"
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/db_xref="taxon:8364"
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Pred. No.
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                                                                                                                                                                928 bp mRNA linear EST 13-JUL-2000 Homo sapiens cDNA clone IMAGE:2959391 5',
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TGas073h08.plkSP6
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                                                Euteleostomi;
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FGas073h08 5',
                                  Homo
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        Contact: Genoscope
Control National de Sequencage
Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
                                                                              Full-length cDNA libraries Unpublished (2001)
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 952)
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High quality sequence stop: 758.
Location/Qualifiers
                                                                                                   Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                         Homo sapiens
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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segref@genoscope.cns.fr,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2959391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="adenocarcinoma cell
/lab_host="DH10B (phage-resistant)
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Pred. No. 33;
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www.genoscope.cns.fr
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image.llnl.gov
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                                                                                                                                           Seq primer: -40M13 1W4. 110.
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                    Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zp29e06.sl Stratagene neuroepithelium (#937231) Homo clone IMAGE:610882 3/, mRNA sequence.
                                                                                                                                                                   his clone is available royalty-free through LLNL;
MAGE Consortium (info@image.llnl.gov) for further i
eq primer: -40Ml3 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Lennon,
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Mammalia; Eutheria;
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                                            /db_xref="taxon:9606"
                                                                 /db_xref="GDB:462614;
                                                                                                                               Location/Qualifiers
                          /clone="IMAGE:610882"
                                                                                     organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 .to 422)
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vas primed with a NotI-oligo(
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/lab_host="DH10B"
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3 c 247 g 184 t 1
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Pred. No. 38;
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T., Favello, A., Gish, W., Ha
                                                                                                                                                                                          gov) for further information.
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sequencing pipeline with 384 multicapillary 10 (11), 1757-1771 (2000)

Itoh, M., Carninci, P., Sugahara

sequencer.

Genome

Res

RIKEN integrated sequence analysis (RISA) system -- 384-format

,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

yenes. Genome Res. . 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu

S., Kawai, J., Okazaki, Y., Muramatsu, M.,

Inoue, Y., Ki

ka,T., Matsuura Kira,A. and

Fax: 01.\*2 J. Fax: 01.\*2 Fax: 01.

Shibata, K., Itoh

Laboratory for Genome Exploration Researd Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Rel 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Tel: 81-45-503-9222

Research (RIKEN)

230-0045, Japan

Contact: Yoshihide Hayashizaki

Exploration Research Group,

RIKEN Genomic

Fax: 81-45-503-9216

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JOURNAL COMMENT
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AUTHORS
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VERSION
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BB628805
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            Unpublished
                                        Muramatsu, M. and Hayashizaki, Y.
                                                     Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y.,
                                                                                         OKazaki
                                                                                                                                 1 (bases 1 to 706)
Arakawa, T., Carninci, P.,
                             RIKEN Mouse ESTs
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                               house mouse
                                                                                                                   Hiramoto; K.,
                                                                  Koya,S., Matsuyama,T., Miyazaki,A.,
aki,Y. Okido,T., Saito,R., Sakai,C.,
Shibata,K., Shinagawa,A., Shiraki,T.
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cDNA clone 9630035G12 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Stratagene neuroepithelium
/dev_stage="Ntera-2/RA neuroepithelial
                                                                                                                                                                                                                                          GI:16466143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.18; Score 34; 54.58; Pred. No.
                                                                                                               Hori, F., Ishli, Y., Ito, M., Kawai,
                         (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                 T., Miyazaki, A., Nomura, K., aito, R., Sakai, C., Sakai, K.,
                                                                                                                                 Fukuda, S.,
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34;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 774) NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizav
                                                                                                                     EST
                                                                                                                                                          mRNA sequence.
BI153642
                                                                                                                                                                              BI153642
602871227F1 NCI_CGAP_Mam2 Mus
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                                                                             Mus musculus
                                                                                                                                     BI153642.1 GI:14613643
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                                                                                                                                                                                                                                                                                                                TTCCAGGTCCCCGGCGGGGTCTGGCCGGAGACAAG 576
                                                                                                                                                                                                                                                                                                                                                        TTGGGCGTGCCCCCGCGAGACTGCTAGCCGAGTAG 194
                                                                                                                                                                                                                                                                                                                                                                                               GCGGTCACCGGAGCGCTACTTCCATGGACAGGCCTGAGGCTTCGAGGCGCCTACTATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified pBluescript KS(+) after bulk excision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="cerebellum"
/dev_stage="16 days neonat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Site_1: SalI; Site_2: BamHI; cDNA library"
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ab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                              Korea Research Institute of Bioscience 52 Eoeun-dong Yuseong-gu, Daejeon 305-3 Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                  K-EST0008231 S2SNU668 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLAM11039 row: e column:
High quality sequence stop: 752.
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                                                                                                                                        21C Frontier Korean EST Project 2001 Unpublished (2002)
                                                                                                                                                                                           Kim, N.S., Hahn, Y., Oh,
Oh, K.J., Cheong, J.E.,
                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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                                 Fax: +82-42-860-4409
                                                                                                   Genome Research Center
                                                                                                                         Contact: Kim YS
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                         Homo sapiens
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yongsung@mail.kribb.re.kr
11 row: D column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Site_2: Not1; Cloned unidirectionally. Primer: Olig Library constructed by Life Technologies. Investigat providing samples: Gilbert Smith, NIH" 222 c 235 g 156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5003119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 67;
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                                                                   lence & Biotechnology 305-333, South Korea
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Matches 52
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                                                                    High quality sequence stop: 575.
Location/Qualifiers
                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                            Contact: Robert Straubberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                NiH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 575)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indee Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NoLI; The poly (A)+ RNA was decapped with Labacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-talled vector. The dT-talled vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion was circularized with E. coli DNA ligase after digestion
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/db_xref="taxon:9606"
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                                                              1. .575
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3913149"
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|_line="SNU-668"
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Pred. No. 75;
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ORIGIN

Query Match Best Local Similarity

> Score 32.8; pred. No. 83

> > DB 13;

Length 655;

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RESULT 12
BI765955/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI765955 mRNA linear EST 25-SEP-2001 603047231F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187631.5',
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1 (bases 1 to 655)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Life Technologies, Inc
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; vector: pCMV-SPORT6; Site_1: NotI;
/note="Gran: uterus; vector: pCMV-SPORT6; Site_1: Oligo dT
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb.
a 201 c 170 g 85 t
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                                                      /note="Organ: pooled colon, kidney, stomach; Vector: pcMv-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA pcMv-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of, 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is stomachs, 62 yo male and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, destroyed upon cloning). Average insert size 1.4 kb, Library is normalized and insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. gruber (invitrogen). Research Genetics tracking code gruber (invitrogen).
                                                                                                                                                                                                                                                                                                                                               'db_xref="taxon:9606"
'clone="IMAGE:5187631"
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     per (invitrogen). Research Geneti
Note: this is a NIH_MGC Library."
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pred. No. 80;
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                                                                                                                                                                                                                                                1 GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT 60

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDEP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDCP from the 1sogenic strain y2; on bw sp, the same strain used for the BDGP's
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and how to order individual BAC clones,
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Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                       TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGC 212
                                           GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bases 1 to 925
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                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rs for hybridization from the BACPAC Resource Center at http://bacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                          /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
a 61 c 61 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                              13.6%;
13.7%;
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                                                                                                                                                                                                                                                                                                          Score 32.8;
Pred. No. 91;
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RESULT 14
BF306437/c
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BC014080/c
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                                   ORGANISM
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                                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                               123 GTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTG 162
                                                                                                                                                                                                                                                                                                    224 CAGGGCATCCAGCACTGTCTGTGACTCTGTAGGGGCCACTGGGGGTTGCTGGGACGTCAGG
                                                                                                                                                                                                                                                                                                                                    63 CGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACCGG 122
                                                                                   Homo sapiens,
BC014080
BC014080.1 GI
                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1048 row: 1 column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1331)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601893322F1 NIH_MGC_17 Homo
                               Homo sapiens.
                                                                      HTC.
                                                                                                                                           BC014080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF306437.1
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                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                GGCCATCACTGGCTGCACTCGCTCCACGGCTGGGGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Site_12: XhoI; cloned into EcoRI/XhoI sites using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
180 c 382 g 147 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4138900"
/clone_lib="NIH_MGC_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "tissue_type="rhabdomyosarcoma"
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                Metazoa;
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                                                                                       GI:17315140
                                                                                                                      2670 bp
clone IMAGE:4309173,
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Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 1e+0
0; Mismatches
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Craniata; V
Catarrhini;
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                                                                                                                        mRNA
mRNA
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s cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                         42;
                  Vertebrata;
   Hominidae;
                                                                                                                                                                                                                                  125
                                                                                                                                                                                                                                                                                                                                                                                                       Length 1331;
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                  Euteleostomi;
                                                                                                                                           HTC
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2:4138900 5',
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ORIGIN
Search completed: July 11, 2003, Job time: 4340:13 secs
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JOURNAL
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Best Local S
Matches 58
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                                                                                                                                                                                         776 CAGGGCATCCAGCACTGTGTGACTCTGTAGGGGCCACTGGGGTTGCTGGGACGTCAGG 717
                                                                                               716 GGCCATCACTGGCTGCACTGGCTGGGGGAATG 677
                                                                                                                                              123
                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                     13.6%;
1 Similarity 58.0%;
58 Conservation
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Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: ggapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone has the following problem: incomplete processing Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. (Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: 1 Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X.; Gupta,J., Ho,S.-I., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R.; Snyder,B., Stantripop,S., Thomas,P.J.,
McDowell,J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                      CGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGGAATTGCCAGGACGACCGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lang, L.-H. and Green, E.D.
                                                                                                                             GTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Library Preparation: Rubin Laboratory
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
uencing Center (NISC),
thersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 2670)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ue Procurement: Louis Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site:
                                                                                                                                                                                                                                                                                                                                                                                                              657
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="primary B-Cells from Tonsils"
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pOTB7"
742 c 774 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="IMAGE: 4309173"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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                           02:26:19
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                                                                                                                                                                                                                                                                                                                                                                                                                   497
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                                                                                                                                                                                                                                                                                                                                          Length 2670;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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241
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3358.597 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_ba:
                                em_htg_vrt:*
em_sy:*
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em_htgo_hum:*
em_htgo_mus:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. Query Match 100 100 100 100 100 9 100 9 100 100 100 100 9 100 100 9 8 88 8 8 1499 1499 1499 1499 멂 HPCBCU5 AX398187 AX419905 AR119855 AR119856 A98437 D88470 AR091903 AR145552 HCU94722 AR153761 AR153763 AR005071 HPCRNADR4 HPCRNAHK5 HPCRNAP10 HPCRNAS45 HPCRNAD HPCRNIND HPCRNAUS HPCRNASW: A98437 Sequence 21 D31724 Hepatitis C AF217300 Hepatitis C L34388 Hepatitis C AX398187 Sequence M84842 Hepatitis C M84849 Hepatitis C M84899 Hepatitis C M84899 Hepatitis C AR095006 Sequence U94722 Hepatitis C AR153761 Sequence AR053071 Sequence AR064510 Sequence AR091903 Sequence AR091903 Sequence E06166 CDNA encod1 E06362 CDNA encod1 E06362 CDNA encod1 AR027784 Sequence AX419905 Sequence AR119855 Sequence AR119856 Sequence AR153763 Sequence U05028 Hepatitis ( E06161 cDNA encodi E06357 cDNA encodi E50749 Vector expr AR095001 Sequence AX282476 Sequence Description E50750 Vector expr AR142355 Sequence AR167008 Sequence NR210663 Sequence L40552 Hepatitis C Human hepat Hepatitis

ALIGNMENTS

ASBULT 1
A98437
LOCUS
DEFINITION
ACCESSION
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SOURCE
ORGANISM A98437 Sequence 2 A98437 A98437.1 unidentified unclassified. unidentified. Landt, O. (bases 1 to 244) 21 from Patent GI:6781538 W09912948

> linear PAT 07-SEP-2000

REFERENCE AUTHORS TITLE Protein-coated polyribonucleic acids, method for the production thereof, and use of the same Patent: WO 9912948-A 21 18-MAR-1999;

JOURNAL

Pred. No. is the number of results predicted by chance to have a

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	Query Match Best Local S Matches 241	5'UTR BASE COUNT ORIGIN	FEATURES.	, [		TITLE C JOURNAL V MEDLINE 9	RS CE	ORGANISM	SON .				Qy 18	Οy 123 Db 123	Db 6	Db x	Query Matc Best Local Matches 2	BASE COUNT ORIGIN	FEATURES SOUICE	
GCAGAAAGCGTCTAGCCA	Similarity 100.0%; Solution 100.0%; P. Conservative 10;	/clone="BULG" 1. 254 46 a 72 c	Location/Qualifiers 1254 /organism="Hepatiti /db_xref="taxon:111	edical School, Seco izuho, Mizuho-ku, N ax:052-852-0849)	2 (bases 1 to 254) Suzuki,K. Direct Submission	lass ased irus 5381	1 (sites) 1 (sites) 1 (sites) 1 (sites) 2 (sit	Hepatitis C virus cDNA to genomic RNA, Hepatitis C virus Viruses; ssRNA positive-strand viruses, Hepacivirus	D31724.1 GI:2388524	D31724	C 241		- p p		1 CCCGGGAGAGCCATAGT		4 4 5	45 a	Location/C 1244 /organism=	LANDT OLFERT (DE)
GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT	Score 241; DB 14; Pred. No. 6.5e-60; 0; Mismatches 0;	6" 82 g 54 t	Location/Qualifiers 1. 254 /organism="Hepatitis C virus" /db_xref="taxon:11103"	Junilited (UI-JUN-1994) Kaoru Suzuki, Nagoya City University Medical School, Second Department of Internal Medicine; 1-Kawasumi Mizuho-ku, Nagoya, Aichi 466, Japan (Tel:052-853-8748, Fax:052-852-0849)	•	ification of hepatitis C virus into on molecular evolutionary analysis Res. 36 (2-3), 201-214 (1995)	, Ohno,T., Suzuki,K.,	NA to genomic RNA, (ive-strand viruses,	nic RNA, 5'UTR,	254 bp RNA			TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG	GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGAGAC	CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTAGTACACCGGAATTGCCAGGACGACC	COMMAND OF THE CHAINS CONTROL OF THE CONTROL OF T	%; Score 241; DB 6; %; Pred. No. 6.5e-60; 0; Mismatches 0;	67 c 81 g 51 t	ocation/Qualifiers  1. 244  'organism="unidentified"	
TGCAGCCTCCAGGACCCCC	Length 254; ; Indels 0; Gaps			Igoya City Universit Pernal Medicine; 1 <sup>1</sup> K Pan (Tel:052-853-87	,	major types and	., Orito,E., Ina,Y.,	clone:BULG. no DNA stage; Flav	clone:BULG:		· ·		GGTACTGCCTGATAGGGTG 	ATTTGGGCGTGCCCCCGCG	ACACCGGAATTGCCAGGAC	GTGCAGCCTCCAGGACCCC	); Length 244; 0); Indels 0; G			
CCT 60	ps 0;			y awasumi, 48,		subtypes		Flaviviridae;		VRL 09-SEP=1997			CTTG 240	AGAC 180      AGAC 180	GACC 120       ACC 120	CCCT 60	Gaps 0;			
RESULT 4 HPCBCU5	Qy 241 Db 244	Qy 18 Db 18	Qy 1: Db 1:	Qy Db	Db 43	Best Local Sin Matches 241;	BASE COUNT ORIGIN	5'UTR	FEATURES Source	JOURNAL	REFERENCE AUTHORS	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	AF217300 LOCUS DEFINITION		Ωу	ОУ	ОУ	Qy	<del>-</del>
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/organism="Hepatitis C virus" /db_xref="taxon:11103" /clone="qott2"	
urce 1. 256	SO
Service, Southampton General Hospital, Southampton, 6YD, United Kingdom	
Direct Submission Submitted (20-DEC-1999) Microbiology, Public Health Laborator	TITLE JOURNAL
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AF217300 DN Hepatitis C virus cl	RESULT 3 AF217300 LOCUS DEFINITION ACCESSION
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses,
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Sequence 64 from Patent WO0220837.
AX398187
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Hepatitis C virus DNA.
Hepatitis C virus
                                                                                                      Patent: WO 0220837-A 64 14-MAR-2002;
Pyrosequencing AB (SE); The Board o
Stanford Junior University (US)
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Identification of hepatitis C virus genotypes
patients in British Columbia, Canada
J. Infect. Dis. 171 (4), 1034-1038 (1995)
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/protein_id="AAA45679.1"
/protein_id="AAA45679.1"
/db_xref="GI:329890"
/translation="MSTNPKPQRKTKR"
91 c 97 g 64 t
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/isolate="D3"
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DNA

Flaviviridae;

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      C 249
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Hepacivirus.
Thases 1 to 321)
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/protein_id="AAA45680.1"
/db_xref="GI:329892"
/translation="MSTNPKPORKTKR"
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/isolate="D6"
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Sequence analysis of the 5' noncoding region of hepatitis C virus
Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)
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/protein_id="AAA45683.1"
/db_xref="GI:329898"
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91 c 97 g 64 t/
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/isolate="DR4"
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Pred. No. 6.5e-60;
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polyprotein. Hepatitis C

(individual\_isolate

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cDNA to genomic

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Hepatitis C

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isolate HK5 5' end.

321 bp ss-RNA HK5 5' untra

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Best Local Sim
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( bases 1 to 321)

1 (bases 1 to 321)

Bukh,J., Purcell,R.H. and Miller,R.H.

Sequence analysis of the 5' noncoding region of hepatitis C virus

Sequence analysis of the 5' noncoding region of hepatitis C virus

( 1992)
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Hepatitis C virus (individual_isolate P10)
Hepatitis C virus
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M8485
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Sequence analysis of the 5' noncoding region of hepatitis C virus
Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)
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/isolate="HK5"
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91 c 97 g 64 t
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/protein_id="AAA45685.1"
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Pred. No. 6.5e-60;
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Hepatitis C virus polyprotein mRNA, 18484840
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                                                                                                                                                                                                   Bukh, J., Purcell, R.H. and Miller, R.H. Sequence analysis of the 5' noncoding proc. Natl. Acad. Sci. U.S.A. 89 (11),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        φ
                                                                                                                                                                                                                                                                                  Hepatitis C virus (individual_isolate S45)
                                                                                                                                                                                                                                                                                                              polyprotein
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                                                                                                                                                                                                                                                         Hepacivirus.
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/db_xref="GI:329904"
/translation="MSTMPKPQRKTKR"
91 c 97 g 64 t
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                                                                                                     /organism="Hepatitis C
/isolate="S45"
/db_xref="taxon:11103"
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/codon_start=1
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/isolate="P10"
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/product="polyprotein"
                         'gene="polyprotein"
                                         'partia
                                                     "polyprotein"
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Pred. No. 6.5e-60;
; Mismatches 0;
                                                                                                                                                                                                      region of hepatitis C virus, 4942-4946 (1992)
                                                                                                                                                                                                                                                                       no DNA stage;
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VRL 19-APR-1994

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gene
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                                                                                                                                                                                                                                    Hepacivirus.

| (bases 1 to 321) |
| (bases 1 to 321) |
| bukh, J., Purcell, R. H. and Miller, R. H.
| Sequence analysis of the 5' noncoding region of hepatitis C virus |
| Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)
                                       Similarity
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                                                                                                                                                                                                                                                                                                                                            polyprotein
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     GCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGACCCCCCCT
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                            clarity 100.0%;
Conservative
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/translation="MSTMPKPQRKTKR"
91 c 97 g 64 t
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                                                                                                                                                        /gene="polyprotein"
283. .321
                                                                                                                                /gene="polyprotein"
/codon start=1
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/isolate="S9"
                                                                                                                           codon_start=
                                                                                                                                                                                  'db_xref="taxon:11103"
|...282
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/db_xref="GI:329908"
/translation="MSTNPKPQRQTNR"
93 c 97 g 64 t
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                          Score 241; DB 14;
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Mismatches 0;
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Hepatitis C
polyprotein m
M84863
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Bukh, J., Purcell, R.H. and Miller, R.H.
Sequence analysis of the 5' noncoding r
Proc. Natl. Acad. Sci: U.S.A. 89 (11),
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                      /product="polyprotein"
/protein_id="AAA4594.1"
/db_xref="Gi:329921"
/translation="MSTNPKPQRKTKR"
/translation="97 g 64 t
                                                                                                                                                                                                                                                                                     /gene="polyprotein"
/codon_start=1
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Pred. No. 6.5e-60;
; Mismatches 0;
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, 4942-4946 (1992)
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188 180

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                                                                                                                                                                                                                               Bukh, J., Purcell, R.H. and Miller, R.H. Sequence analysis of the 5' noncoding region of hepatitis C virus Proc. Natl. Acad. Sci. U.S.A. 89 (11), 4942-4946 (1992)
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Bukh, J., Purcell, R.H.
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Hepatitis C virus (individual_isolate US3)
Hepatitis C virus
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Hepatitis C virus isolate US3 5' untranslated region
polyprotein mRNA, 5' end.
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                                                 TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG 240
                                                                                                                                                                          CCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGGACGACC
                                                                                                                    GGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCGCGGAGAC 180
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                         C 241
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                                                                                                                                                                                                                                                                                                                                           translation="MSTNPKPQRKTKR"
91 c 97 g 64 t
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283. .321
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                                                                                                                                                                                                                                                                        0;
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Pred. No. 6.5e-60;
; Mismatches 0;
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RESULT 15 HPCRNAUS6

Search completed: July 10, 2003, Job time: 2092.31 secs

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BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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Matches 241; Conserv
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Hepatitis C virus isolate polyprotein, 5' end.
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                                                         TGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGGGTGCTTG
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/isolate="US6"
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/codon_start=1
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Pred. No. 6.5e-60;
); Mismatches 0;
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